

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 19, 2003, 15:40:25 ; Search time 4747 Seconds

(without alignments)  
5225.460 Million cell updates/sec

Title: US-09-494-297-2

Perfect score: 3945  
Sequence: 1 MKTRFPNKNTLNTQTVLS.....IAGISLGIWGIHTIRIKHD 757

## Scoring table:

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Searched: 32997241 seqs, 16383922548 residues

Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

RESULT 1

US-09-494-297-1

Sequence 1, Application US/09494297

GENERAL INFORMATION:

APPLICANT: POBIELESKI, ANDREAS

TITLE OF INVENTION: COLLAGEN-BINDING PROTEINS FROM STREPTOCOCCUS PYOGENES

FILE REFERENCE: P06628050/BAS

CURRENT APPLICATION NUMBER: US/09/494, 297

CURRENT FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 2274

TYPE: DNA

ORGANISM: Streptococcus pyogenes

US-09-494-297-1

## Alignment Scores:

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Score: 3945.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 21

Length: 2274

Matches: 757

Conservative: 0

Mismatches: 0

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DB	61	AAAACCAAAACAGATTACTGCTACCTTAAAGGAGCTTTTAATGATCTTCGCTTG	120
QY	41	ValThrSerMetValGlyAlaLysThrValPheGlyLeuValGlySerThrProAsn	60
DB	121	GTAACCTTCATGGTGGTGGTGAACGCTTTTGGTTAGTAAATCTCGAGCCCAAC	180
QY	61	AlaIleAsnProAspSerSerSerGluTyrArgTyrPtyGlyTyrGlySerTyrValArg	80
DB	181	GCATTAATATCCAGATTAAAGTTGCGAATACAGATGATGATGATGATGATGATGATG	240
QY	81	GlyHisProTyrTyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeuGly	100
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QY	161	AsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuLupProLeuAsnAlaIle	180
DB	481	AATGACATCCAAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG	540
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QY	221	ArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnVal	240
DB	661	CGTCAAGCTTTGAAGCAACTGATGATGATGATGATGATGATGATGATGATGATGATG	720
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DB	781	GGATACCAAAATCTTTGAGTGTGTTAGTCTTACTTAACCAACCACTCAGAGAGAC	840
QY	281	ProPheMetProProAsnGlnProGlnThrThrSerValLeuIleArgLysTyrAlaIle	300
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RESULT 2
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; APPLICANT: PODBIELSKI, ANDREAS
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; FILE REFERENCE: P06628US0/BAS
; CURRENT APPLICATION NUMBER: US/09/494,297
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-09-494-297-3

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Best Local Similarity: 54.53% Mismatches: 192
Query Match: 49.82% Indels: 34
DB: 21 Gaps: 16

US-09-494-297-2 (1-757) x US-09-494-297-3 (1-2229)
QY 20 SerLysAsnSerLysArg-----PheThrValaThrLeuValaGlyPheLeuMetIle 37
DB 31 AGCGCTAACCAACAAACGACGACAAACGACGATCGGATTAAGTATTTTGAAGCTTT 90
QY 38 PheAlaLeuValaThrSerMetValaGlyAlaLysThrValaPheGlyLeuValaGluSer 57
DB 91 GTAGCTGATGATGATAGTATGAGTTTCTATACAGAGCGTGTGAGAGCTGAAGAACATCA 150
QY 58 ThrProAsnAlaIleAsnProAspSerSerSerGluTyrArgTyrThrGlyGluGluSer 77
DB 151 GTACCAAAAT-----AGACAAAGCTCAATTCAGATTAACCTGCTATGCTATATCT 204
QY 78 TyrValaArgGlyHisProTyrTyrLysGlnPheArgValaAlaHisAspLeuArgValaAsn 97
DB 205 TATCTTAAAGCTTACCACAGACTATAGTCCGTTAAAGACTTACCATAATTTAAAGATTAAT 264
QY 98 LeuGluGlySerArgSerTyrGlnValaTyrCysPheAsnLeuLysAlaPheProLeu 117
DB 265 TTAGAGGGAAGATTAAGATTAACAGCATCTCTTAAATTTAAACAAACATTTTCCATCC 324
QY 118 GlySerAspSerSerValaLysTyrTrpTyrLysHisAspGlyIleSerThrLysPhe 137
DB 325 AAGTCAGATAGGTTAGATCAACAATGGATTAATAAACTTGGAAGGAACTTAATGAACCTTT 384
QY 138 GluAspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAla 157

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QY 527 AsplysleuLysAspTyrHisGlyAspMetAsnSerThrLeuAlaValAla 546
Db 1230 ----- 1230
QY 547 LysIleLeuValGluTyrAlaGlnAspSerAsnProGlnLeuThrAspLeuAspHe 566
Db 1231 ----- 1231
QY 567 PheIleProAsnAsnLysTyrGlnSerLeuIleGlyThrClnIlePheIleAsp 586
Db 1276 ----- 1276
QY 587 LeuValAspIleIleArgMetGluAspLysGluValIleProValThrHisAsnLeu 606
Db 1297 ----- 1297
QY 607 ThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGlu 626
Db 1330 TCAGGTTTACAGTACAGAGGTCAGTCGGTGAATGACAAATTCAGAGATAGTGTCT 1389
QY 627 IleGluLeuLysAsnAsnLysGlnGlnLeuLeuSerGlnThrValLysThrAspLysThr 646
Db 1390 ACCCAATTAATTAATTCGAAACGCTGATTTGACGCGAAAGAGTTACCTGCTCACTATG 1449
QY 647 AsnLeuGluPheLysAspGlyLysAlaThrIleAsn-----LeuLysHisGlyGluSer 664
Db 1450 GAGTTCGTCATTCATCTGTGTAA--ACTATTAGTACATGATTTTCAGATGACACAAGT 1506
QY 665 LeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGluThrAspSerGlu 684
Db 1507 AAGATTTCACCTGATGCGAGGAAATATACATTT--GTCGAAACCGCAGCACCAGAC 1563
QY 685 GlyTyrLysVal-----LysValAsnSerGlnGluValAlaAsnAla 698
Db 1564 GGTATGAGGTAGCAACTGCTATACCTTACAGTTAATGACAA-----GGTCAGCTT 1617
QY 699 ThrValSerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGlu 718
Db 1618 ACTGTAATGCGCAAAACAACTAAAGGTACGCTCATATGTCATGTTGCTTGTCAAG 1677
QY 719 ProValAlaProThrGly-----ValAspGlnLysIle 729
Db 1678 CCAACTAAGGTTACAGTCACTTATTTGATTGAAGAAAGCTT 1722

RESULT 4
US-09-134-000-2717
; Sequence 2717, Application US/09134000A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
; FILE REFERENCE: GTC-005
; CURRENT APPLICATION NUMBER: US/09/134, 000A
; CURRENT FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 6810
; SEQ ID NO 2717
; LENGTH: 3465
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000-2717

Alignment Scores:
Pred. No.: 8, 26e-07 Length: 3465
Score: 205.00 Matches: 170
Percent Similarity: 35.37% Conservative: 85
Best Local Similarity: 23.58% Mismatches: 236
Query Match: 5.20% Indels: 231
DB: 16 Gaps: 43

US-09-494-297-2 (1-757) x US-09-134-000-2717 (1-3465)
QY 88 PheArgValAlaHisAspLeuArgValAlaAsnLeuGluGlySer-----ArgSerTyrGln 105

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Db 1781 TTCAGGTTCAACATTAA--CCAGAAAGTGTGCTAACGCGGCTCAATTAATAGTAGAG 1839
QY 106 ValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerValLysLys 125
Db 1840 ATTTAT-----TTGGTTAAACGGCAAGAAATTCAAAT 1872
QY 126 TrpTyrLysLysHisAspGlyIleSerThrLysPheGluAsp----- 139
Db 1873 CATTAATCAAGTACGT-----ATTCAACAGAGATCGAAACCTTCAACCTGATTTTGG 1926
QY 140 TyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMet 159
Db 1927 TATCAATGAATGTTGGCAACAGTTTCAGCCATTGACCAAGGCCCCCTGAAAAAGTTGAT 1986
QY 160 TyrAsnGlyHisProLysAsnAlaAsnGlyIleMetGlnGlyLeuLeuProLeuAsnAla 179
Db 1987 TTT-----GGGGTTCCTCGGAAACACCT-----GGC 2016
QY 180 IleArgValThrGlnGluAlaValTyrTyrTyrSerAspAsnAlaProIleSerAsnPro 199
Db 2017 GTCAAGTTAAAGCTGAAGAAATCTGGGAAGATATGATCAAGACCGCAAGTGGCCA 2076
QY 200 AspGluSerPheLysArgLysGluSerGluSerAsnLeuValSerThrSer----- 215
Db 2077 GATTAATGTGATTTTATGAATTTAGTAAAGCAAGTACGACACAGCCAACTGGCAAACT 2136
QY 216 -----GlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeu 232
Db 2137 GGGTATATTAAATTAATTCAAAACCCGAAATATGATACCAAGATAGTTGGGCGCCAAAAT 2196
QY 233 AlaThrLysMetProLysGlnValProAspAspPheGln-----LeuSerIlePheGlu 250
Db 2197 GTAACCAACTTCCAAACCGCGGATGAAGCTATCAAGAAAGTTTGGGCTTCCCAA 2256
QY 251 SerGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuSerGlyGlyLeu 270
Db 2257 TACAAACATCAAGCAAGACCTTTCAT-----TATCAAAACAAACCCGTGAATTAGCA-- 2307
QY 271 ValProThrLysProProThrProGlyAspProProMetProProAsnGlnProGlnThr 290
Db 2308 GTTCTCGTTTACAGTCAAGAAAAATCGACGATACTACTTGGAAACAAACGAGCGCTTC 2367
QY 291 ThrSerVal-----LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeu 307
Db 2368 AAGCCATTAGATTAAAGTAATCAAAATTTCTCTCCAGGTGAG-----AAAACTTA 2421
QY 308 GluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPhe 327
Db 2422 GTGGGAGCCGCTCTTGAATTTGAGTGAATAATGTT-----CAACCAACATTTAGT 2472
QY 328 SerSerAspAsp-----IleGlyGluArgIleGluLeuSerAspGly---Thr 342
Db 2473 GACAATAAAGATGATGATATCTCTTCCCAAAAGATGTGCGCTTACAAAAGGGAGACC 2532
QY 343 TyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPhe 362
Db 2533 TATACATTAACTGAATTAAGACCTCGACGACATGATAGGCAAGAAACGACTTGG 2592
QY 363 LysValGluAla-----GlyLysValTyrThrIleIleAspGlyLysGlnIleGlu 379
Db 2593 CAATATGAGGTGAGTACAGCAAGCAAGTA-----AGCATGATGACAAAGAGTACC 2646
QY 380 AsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGluGlu 399
Db 2647 ACCACAAATCAAGATTAT-----CCATTGGAATTTGA-----AATTAATTTCTCT 2694
QY 400 PheSerVal-----LeuThrThrGln-----AsnTyrAlaLys 410
Db 2695 TTGCCAATCAGATTAGAAATATACCAATGCAAAATGCGAAACAACTGATTAGCAGAG 2754
QY 411 PheTyrTyrAla-----LysAsnLysAsnGlySerSerGlnValValTyrCysPhe 427

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Db      2755 GCGACTTTTGGCTTGCAGAAAGAAAAATGCTCAGAGGAGTTACCAAACTGTGGCAACTCAA 2814
Qy      428 AsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrMetThrProAsp 447
Db      2815 AAAACAGAT----- 2823
Qy      448 PheThrGluGluValLysThrHisIleAlaGlyArgAspLeuPheLysThr 467
Db      2824 ---ACTACAGAG----- 2832
Qy      468 ValLysProArgAspThrAspProAspThrPheLeuLysHisIleLysValIleGlu 487
Db      2833 -----TTGACCTATTTT---AAATATGATGA 2856
Qy      488 LysGly---TyrArgGluLysGlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGln 506
Db      2857 CCTGTGAGTATCA-----ATCGTGACACATCAGCA-----CCA 2892
Qy      507 LeuArgAlaIleThrGlnLeuAlaIleTyrThrPheThrAspSerAlaGluLeuAspLys 526
Db      2893 TTAGGCTACGACACTCTTCTGCAAAATTGATTAATTACT-----GTTGATTA 2940
Qy      527 AspLysLeuLysAspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAla 546
Db      2941 -----TATGGGAAA----- 2949
Qy      547 LysIleLeuValGluTyrAlaGln-----AspSerAsnProProGlnLeuThrAsp 563
Db      2950 -----ATTCACTATGACAGCAAAATATGACAAATATGACGCGCAGATGACACA--- 2997
Qy      564 LeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGlnThrHis 583
Db      2997 ----- 2997
Qy      584 ProLysAspLeuValAspIleIleArgMetLysAspLysGluValIleProValThr 603
Db      2998 -----CTGACA 3003
Qy      604 HisAsnLeuThrLeuArgLys-----ThrValThrGlyLeuAlaGlyAspArgThr 620
Db      3004 CATCAAAATATATTTGAAACCTTTTGACTTACAGTTCATATAAAAAAGCCGAAATACAGACG 3063
Qy      621 LysAspPheHisPheGluIleGluLeuLysAsnLysGlnGluLeuLeuSerGlnThr 640
Db      3064 -----CCACTTAAGACGACGAAATTCCTGTTAAACAGCA----- 3096
Qy      641 ValLysThrAspLysThrAsnLeuGluPhe---LysAspGlyLysAlaThr----- 656
Db      3097 -----CCAGATACGAGATATGAAATTACCAAAAGATGGCAAAAGAACGATACCTTT 3147
Qy      657 -----IleAsnLeuLysHisGlyGlu---SerLeuThrLeuGlnGlyLeuProGluGly 673
Db      3148 GTTTTGAACAACTTAAACCGAGGAAATATGTTCTAACAGAAACCTTTACCCGACAAAGCA 3207
Qy      674 TyrSerThrLeuValLysGluThrAsp-----SerGluGlyTyrLysValVal 690
Db      3208 TATACGGGTTAAAGAACCAATCGAATTAATTAATCTGTAAGATGTTCACTACGCACTA 3267
Qy      691 AsnSerGlnGluValAlaAsnAlaThrValSer-----LysThrGlyIleThrSer 707
Db      3268 GATGGGAAAGAGTACGAGATGTTTAATTTCTGGAGAGAAATATCAAAATTAATCTTA 3327
Qy      708 AspGluThrLeuAlaPheGluAsnLysGluProValValProThrGlyValAspGln 727
Db      3328 GACCTTACG-----AACCAAGCAAAAGCTTCCTTACCTGAACAGTGGGATAGCA 3378
Qy      728 LysIleAsnGlyTyrLeuAlaLeuIle-----ValIleAlaGlyIleSerLeuGly 744
Db      3379 CGCTTGCTGTTTACTTGATAGCGATTAGTCAATTCGTGATGAGGGGTTTATCTCTTT 3438
Qy      745 Ile 745
Db      3439 ATT 3441

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RESULT 5
US-09-134-000C-2717
; Sequence 2717, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIORITY FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2717
; LENGTH: 3465
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2717

Alignment Scores:
Pred. No.: 8,266-07 Length: 3465
Score: 205.00 Matches: 170
Percent Similarity: 35.37% Conservative: 85
Best Local Similarity: 23.568 Mismatches: 236
Query Match: 5.208 Indels: 231
DB: Gaps: 43

US-09-494-297-2 (1-757) x US-09-134-000C-2717 (1-3465)

Qy      88 PheArgValAlaHisAspLeuArgValAsnLeuGluGlySer-----ArgSerTyrGln 105
Db      1781 TTCAGGTTCAACAACTTA-CCAGAAAGTGCCTGCTACAGCGCGTACATTAATTAATAGTAAAG 1839
Qy      106 ValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLys 125
Db      1840 ATTTAT-----TTGGTTAAAGGCAAGAAATTCAAATT 1872
Qy      126 TrpTyrLysLysHisAspGlyIleSerThrLysPheGluAsp----- 139
Db      1873 CATTAATCAAGTACGT-----ATTCAACAGAGTCAAGAAACCTTCAACCTGATTTTGG 1926
Qy      140 TyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMet 159
Db      1927 TATCAAAATGAATGTCGAGCAACCTTTCAGCCATTAGCCACGCGCCCTGAAGAAAGTTGAT 1986
Qy      160 TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAla 179
Db      1987 TTT-----GGGGTTCCTTGGGAAAGCACCT-----GGC 2016
Qy      180 IleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsnPro 199
Db      2017 GTGAAGTTAAACGTGAAGAAATATCTGGAGAGATGATCAAGAACCCGACAAAGTCGGCCA 2076
Qy      200 AspGluSerPheLysArgGluSerGluSerAsnLeuValSerThrSer----- 215
Db      2077 GATATATGATTTATGAATTAATGAGAAAGCAAGTAAGTACACACGACCACTGGCAACT 2136
Qy      216 -----GlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeu 232
Db      2137 GGGTATATTAATTAATTTCAAAACACGAAATATGACACCAATAGTTGGAGCGCAAAAT 2196
Qy      223 AlaThrLysMetProLysGlnValLeuProAspAspPheGln-----LeuSerIlePheGlu 250
Db      2197 GTAACCCAACTTCCAAACCGCGGATGAAAGCTATCAAGAAAGTCTTGGGCTTCCCA 2256
Qy      251 SerGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeu 270
Db      2257 TACAACAATCAAGCAAGCAAGCTTTCAT-----TATCAAAACACCCGTAATTAACA--- 2307
Qy      271 ValProThrLysProProThrProGlyAspProMetProProAsnGlnProGlnThr 290

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Db 2308 GTTCCGTGTTACAGTCAAGAAAAATCGACGATCTACTTGGAAGAAACAGCAAGCACTTC 2367  
 QY 291 ThrSerVal-----LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeu 307  
 Db 2368 AACCCATTAGATTAAAGTAATCAAAATCTTCCACAGTGG-----AAAACCTTA 2421  
 QY 308 GtUGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPhe 327  
 Db 2422 GTGGGAGCCCTCTTGAATTGAGTGTGAATAATGTT-----CAAAACACATTAGTG 2472  
 QY 328 SerSerAsnAsp-----IleGlyLysArgLysIleGlyLeuSerAspGly-----Thr 342  
 Db 2473 GACAAATAAGATGCTAGCTATTCCTCCCAAGAAAGATGGCCCTACAAAAAGGGAACGC 2532  
 QY 343 TyrThrLeuThrGlnLeuAsnSerProAlaGlyTyrSerIleAlaGlnProIleThrPhe 362  
 Db 2533 TATACATTACGTAAAGTAAGAACCTCGACGACATGAGTTAGCAAGAAAGACACTGG 2592  
 QY 363 LysValGluAla-----GlyLysValTyrThrIleIleAspGlyLysGlnIleGlu 379  
 Db 2593 CAATTGAGGTGAGTACGACAAAGCAAGTA-----AGCATGATGACAAAGATGACC 2646  
 QY 380 AsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGlnGlu 399  
 Db 2647 ACCACAAATCAAGTTAT-----CCATTGGAATTTGAA-----AATAAATTTCTCT 2694  
 QY 400 PheSerVal-----LeuThrThrGln-----AsnTyrAlaLys 410  
 Db 2695 TTCCCAATTCAGATTAGAAAATACACCATCAAAATGGCAAAAGCAAGCACTTAGCAGAG 2754  
 QY 411 PheTyrTyrAla-----LysAsnLysAsnGlySerSerGlnValTyrCysPhe 427  
 Db 2755 GCGACTTTGGCTTGCAAGAAAGAAATGCTCAAGCAAGTACCAAACTGGGCAACATCAA 2814  
 QY 428 AsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrMetThrProAsp 447  
 Db 2815 AAAACAGAT----- 2823  
 QY 448 PheThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPheLysTyrThr 467  
 Db 2824 ---ACTACAGGA----- 2832  
 QY 468 ValLysProArgAspThrAspProAspThrPheLeuLysHisIleLysLysValIleGlu 487  
 Db 2833 --- 2856  
 QY 488 LysGly---TyrArgGluLysGlyGlnAlaIleGlyLysSerLysLeuThrGln 506  
 Db 2857 CCTGGTGAGTATCGA-----ATGGTGAAACAATCAGCA-----CCA 2892  
 QY 507 LeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLys 526  
 Db 2893 TTAGCGTAGACACCTCTGCTGGAATTAATGATTTACT-----GTTGATTA 2940  
 QY 527 AspLysLeuLysAspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAla 546  
 Db 2941 --- 2949  
 QY 547 LysIleLeuValGluTyrAlaGln-----AspSerAsnProProGlnLeuThrAsp 563  
 Db 2950 --- 2997  
 QY 564 LeuAspPhePheIleProAsnAsnLysTyrGlnSerLeuIleGlyThrGlnTyrHis 583  
 Db 2997 --- 2997  
 QY 584 ProGluAspLeuValAspIleIleArgMetGluAspLysGluValIleProValThr 603  
 Db 2998 --- 3003  
 QY 604 HisAsnLeuThrLeuArgLys-----ThrValThrGlyLeuAlaGlyAspArgThr 620  
 Db 3004 CATCAAAATAATTTGAACCTTTTGACTTAACAGTTCAATAAAACCCGATTAATCAGACG 3063

QY 621 LysAspPheHisPheGluIleGlyLeuLysAsnAsnLysGlnIleuLeuSerGlnThr 640  
 Db 3064 -----CCACTTAAGAGAGCAAAATTCGCTTAACAGCA----- 3096  
 QY 641 ValLysThrAspLysThrAsnLeuGluPhe---LysAspGlyLysAlaThr----- 656  
 Db 3097 -----CCAGATACGGAATATTGAATTACCAAAAGATGCAAAAGCAAGCACTATT 3147  
 QY 657 -----IleAsnLeuLysHisGlyGlu---SerLeuThrLeuGlnIleuProGluGly 673  
 Db 3148 GTTTTGAATAACTTAATAACAGGGAATATGTTCTTAACAGAAACCTTTACCCAGAGGA 3207  
 QY 674 TyrSerTyrLeuValLysGluThrAsp-----SerGluGlyTyrLysValLysVal 690  
 Db 3208 TATCAGGCGCTTAATAAGAACCAATCGAATTAATTAATGTAAGATGTTGACGACAGATA 3267  
 QY 691 AsnSerGlnGluValAlaAsnAlaThrValSer-----LysThrGlyIleThrSer 707  
 Db 3268 GATGGGGAAAGTAAGTACGACATGTTTAATTTCTGAGAGAGAATAATCAATTAATCTT 3327  
 QY 708 AspGluThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAspGln 727  
 Db 3328 GACGTTACG-----AACCAAGCAAAAGTTCTTTACTGAAACCTGGTGCAATPAGA 3378  
 QY 728 LysIleAsnGlyTyrLeuAlaLeuIle-----ValIleAlaGlyIleSerLeuGly 744  
 Db 3379 CGCTTGGCTTTACTTGATAGGCAATTAGACATTGCTGATACGGGTGTTATCTCTTT 3438  
 QY 745 Ile 745  
 Db 3439 ATT 3441

RESULT 6  
 US-10-434-665-2717  
 ; Sequence 2717, Application US/10434665  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn Doucette-Stamm et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
 ; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: PAT#03-09  
 ; CURRENT APPLICATION NUMBER: US/10/434,665  
 ; CURRENT FILING DATE: 2003-05-14  
 ; PRIOR APPLICATION NUMBER: US 09/134,000  
 ; PRIOR FILING DATE: 1998-08-13  
 ; PRIOR APPLICATION NUMBER: US 60/055,778  
 ; PRIOR FILING DATE: 1997-08-15  
 ; NUMBER OF SEQ ID NOS: 6812  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2717  
 ; LENGTH: 3465  
 ; TYPE: DNA  
 ; ORGANISM: Enterococcus faecalis  
 ; US-10-434-665-2717

Alignment Scores:  
 Pred. No.: 8,26e-07 Length: 3465  
 Score: 205.00 Matches: 170  
 Percent Similarity: 35.37% Conservative: 85  
 Best Local Similarity: 23.58% Mismatches: 236  
 Query Match: 5.20% Indels: 231  
 DB: 53 Gaps: 43

US-09-494-297-2 (1-757) x US-10-434-665-2717 (1-3465)

QY 88 PheArgValAlaHisAspLeuArgValAsnLeuGluGlySer-----ArgSerTyrGln 105  
 Db 1781 TTCAGGCTTCAAAACATTAA-CCAGAAAGTGTGCTTAACAGCGGCTCAATTAATGATTAATGAG 1839  
 QY 106 ValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLys 125  
 Db 1840 ATTAT-----TTGGTAAAGGCGCAAGAAATTCAAATT 1872



QY 126 TrpTyrLysLysHisAspGlyIleSerThrLysPheGluAsp----- 139  
 DB 1873 CATATCAAGTACGCT-----ATTCAAACAGAGTCAGAAAACCTTCAAACCTGATTTTGG 1926  
 QY 140 TyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMet 159  
 DB 1927 TATCAAAATGATGTCGCGACACAGCTTTCAGCATTTAGCCAGCGCCCGCAAAAAGTTGAT 1986  
 QY 160 TyrAsnGlnHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGlnProLeuAsnAla 179  
 DB 1987 TTT-----GGGGTTCCTTCGGGAAAAAGCACCT-----GGC 2016  
 QY 180 IleArgValThrGlnGluAlaValTyrPyrTyrSerAspAsnAlaProIleSerAspPro 199  
 DB 2017 GTGAAGTTAAACGTGAATAAAATCTGGAGAGATGATGATCAAGACCCGACAACTCGGCA 2076  
 QY 200 AspGluSerPheLysArgGluSerGluSerLysLeuValSerThrSer----- 215  
 DB 2077 GATATGATGATTTTGAATAATTAGTAAAGCAAGTAACTGACACAGCCCACTGGCAACT 2136  
 QY 216 -----GlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeu 232  
 DB 2137 GGGTATATTAATTAATTAACAAACAGAAATGATACCAACATAGTTGGAGCGCAAAAT 2196  
 QY 233 AlaThrLysMetProLysGlnValProAspAspPheGln-----LeuSerIlePheGlu 250  
 DB 2197 GTAAACCACTTCCAAACCGCGATGACAGTATCAAGAAAGTTCTGGGCTTCCCA 2256  
 QY 251 SerGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyLysLeu 270  
 DB 2257 TACAACATCAAGCAAGCAAGCTTCAAT-----TATCAACACACCCGCAATTTAGCA--- 2307  
 QY 271 ValProThrLysProProThrProGlyAspProPheMetProProAsnGlnProGlnThr 290  
 DB 2308 GTTCTCGTTCAGTCAAGAAAAAATCGACATCTACTCTGAAAAACACAGACAGCTTC 2367  
 QY 291 ThrSerVal-----LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeu 307  
 DB 2368 AAGCATTAAGATTAAAGTAAATCAAAATCTTCTCCTAGGTGAG-----AAAACCTTA 2421  
 QY 308 GluGluAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPhe 327  
 DB 2422 GTGGAGAGCCGCTTGAATGAGTGTAAATGTT-----CAAAACAATTTAGTG 2472  
 QY 328 SerSerAsnAsp-----IleGlyLysArgIleGluLeuSerAspGly---Thr 342  
 DB 2473 GACATTAAGATGAGTACCTATCTCTGCCAAAAGATGCGCTTCAAAAAGGAGACGC 2532  
 QY 343 TyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPhe 362  
 DB 2533 TATACATTAAGTGAAGTAAAGACACCTGACAGCATGAGTAAAGCAAAAACGACTTGG 2592  
 QY 363 LysValGluAla-----GlyLysValTyrThrIleIleAspGlyLysGlnIleGlu 379  
 DB 2593 CAATTTGAGTGTAGTACCAAGCAAGTA-----AGCATGATGACAGCAAGATGACGC 2646  
 QY 380 AsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGluLeu 399  
 DB 2647 ACCACAAATCAAGTTATT-----CCATTGAAATTTGAA-----AATTAATTTCTTCT 2694  
 QY 400 PheSerVal-----LeuThrThrGln-----AsnTyrAlaLys 410  
 DB 2695 TTGGCAATCAGAAATTAGAAATACACCATGCAAAATGCGCAACAAAGTAACTTACAGAG 2754  
 QY 411 PheTyrTyrAla-----LysAsnLysAsnGlySerSerGluValAlaTyrCysPhe 427  
 DB 2755 GCGACTTTTCGCTGCAAGAAAGAAATGCTCAAGGAAGTACCAAACTGCGCAACTCAA 2814  
 QY 428 AsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrMetThrProAsp 447  
 DB 2815 AAAACAGAT----- 2823  
 QY 448 PheThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPheLysTyrThr 467

DB 2824 ---ACTACAGCA----- 2832  
 QY 468 ValLysProArgAspThrAspProAspThrPheLeuLysHisIleLysValIleGlu 487  
 DB 2833 -----TTGACCTTAATTT---AAATATGTCGA 2856  
 QY 488 LysGly---TyrArgGluLysGlyGlnAlaIleGluTyrSerGlyLeuThrGln 506  
 DB 2857 CCTGTGAGTATGCA-----ATGGTGAACATCAGCA-----CCA 2892  
 QY 507 LeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLys 526  
 DB 2893 TTAGGCTACGACACTCTTCTCGGAATTAATGATTAATTAAT-----GTGATTA 2940  
 QY 527 AspLysLeuLysAspTyrHisGlyPheGluAspMetAsnAspSerThrLeuAlaValAla 546  
 DB 2941 -----TATCGAAA----- 2949  
 QY 547 LysIleLeuValGluTyrAlaGln-----AspSerAsnProProGlnLeuThrAsp 563  
 DB 2950 -----ATTCACATATGACAGCAAAAATATTTGAAGAAATGCGCCAGAAATGAGCA--- 2997  
 QY 564 LeuAspPhePheIleProAsnAsnLysTyrGlnSerLeuIleGlyThrGlnThrHis 583  
 DB 2997 ----- 2997  
 QY 584 ProGluAspLeuValAspIleIleArgMetGluAspLysGluValIleProValThr 603  
 DB 2998 -----CTGCA 3003  
 QY 604 HisAsnLeuThrLeuArgLys-----ThrValThrGlyLeuAlaGlyAspArgThr 620  
 DB 3004 CATCAAAATTAATTTGAACCTTTGACTTACACAGTTCATAAAAAGCGATATTCAGACG 3063  
 QY 621 LysAspPheHisPheGluIleGluLeuLysAsnLeuLysGlnGluLeuLeuSerGlnThr 640  
 DB 3064 -----CCACTTAAGAGAGCAAAATTCCTTTAAACAGCA----- 3096  
 QY 641 ValLysThrAspLysThrAsnLeuGluPhe---LysAspGlyLysAlaThr----- 656  
 DB 3097 -----CCAGATACGAGATATGCAATTTACCAAAAAGATGCGCAAAAGCAAGATCTTT 3147  
 QY 657 -----IleAsnLeuLysHisGlyLys---SerLeuThrLeuGlnGlyLeuProGluGly 673  
 DB 3148 GTTTTGAACCTTAATAACCAAGCAAAATATGTTCTTAACAGAAACCTTTACCGCAAGAGCA 3207  
 QY 674 TyrSerTyrLeuValLysGluThrAsp-----SerGluGlyTyrLysValLysVal 690  
 DB 3208 TATCAGGGGCTTAAAGAACCAATGCAATTAATTTCTGAAGATGCTTCAGTCAAGATA 3267  
 QY 691 AsnSerGlnGluValAlaAsnAlaThrValSer-----LysThrGlyLysThrSer 707  
 DB 3268 GATGGGGAAGAAAGTGAAGATGTTTAATTTCTGAGAGAGAGAAATATCAAAATTCCTTTA 3327  
 QY 708 AspGluThrLeuAlaPheGluAsnAsnLysGluProValAlaProThrGlyValAspGln 727  
 DB 3328 GACGTTAG-----AACCAAGCAAAAGGCTTCTTAACCTGAACAGTGGTGCATAGCA 3378  
 QY 728 LysIleAsnGlyTyrLeuAlaLeuIle-----ValIleAlaGlyLysSerLeuGly 744  
 DB 3379 CGCTTCGCTGTTTACTTATGACCATTTAGTACATTCGATACGCGGCTTATCTCTTT 3438  
 QY 745 Ile 745  
 DB 3439 ATT 3441  
 RESULT 7  
 US-09-070-927-45  
 ; Sequence 45, Application US/09070927  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Charles Kunsch  
 ; APPLICANT: Patrick J. Dillon

```

APPLICANT: Steven C. Barash
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 15614 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-070-927-45

```

```

Alignment Scores:
Pred. No.: 3.46e-05 Length: 15614
Score: 196.00 Matches: 165
Percent Similarity: 35.57% Conservative: 89
Best Local Similarity: 23.11% Mismatches: 245
Query Match: 4.97% Indels: 216
DB: Gaps: 41
US-09-494-297-2 (1-757) x US-09-070-927-45 (1-15614)

```

```

QY 88 PheArgValAlaHisAspLeuArgValAsnLeuGluGlySer-----ArgSerTyrGln 105
Db 9047 TTCAGGTTCAACATTA-CCAGAAAGTGTCCCTAACAGCGCTACAAATTACTAATGAG 9105
QY 106 ValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerValLysLys 125
Db 9106 ATTAT-----TTGGTTAAGGCAAGAAATTCAATT 9138
QY 126 TrpTyrLysHisAspGlyLeuSerThrLysPheGluAsp----- 139
Db 9139 CATTAACAGTACT-----ATTCAACAGAGATCAGAAACTTCAAACTGATTTTGG 9192
QY 140 TyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMet 159
Db 9193 TATCAATGAAATGCTGGACACGTTTCAGCCATTAGCCAGCGCCCTGAAAAAGTTGAT 9252
QY 160 TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAla 179
Db 9253 TTT-----GGGGTTCCTCGGGAAGACACT-----GGC 9282
QY 180 IleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsnPro 199
Db 9283 GTCAAGTTAAAGCTGAAAAAATCTGGGAAGAGATATGATCAAGACCCGACAAAGTGGCCA 9342
QY 200 AspGluSerPheLysArgGluSerGluSerAsnLeuValSerThrSer----- 215

```

```

Db 9243 GATAATGTGATTTATGAATTTAGTAGAAGACAGTACTGACACAGCAACTGGCAAACT 9402
QY 216 -----GlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeu 232
Db 9403 GGGTATATTAATATATCAAAACAGAAATGATATACGCAATAGTTGGGCCCAAAAT 9462
QY 233 AlaThrLysMetProLysGlnValProAspPheGln-----LeuSerIlePheGlu 250
Db 9463 GTAAACCACTTCCAAACACCGGATGAAAGCATATCAAAAGTTCTTGGGCTTCCCAA 9522
QY 251 SerGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuSerGlyGlyLeu 270
Db 9523 TACAACAATCAAGACAGACCTTCAAT-----TATCAACAACCCGTGAATAGCA--- 9573
QY 271 ValProThrLysProProThrProGlyAspProProMetProProAsnGlnProGlnThr 290
Db 9574 GTTCTGGTTACAGTCAAGAAAAATCGACGATACTACTTGAAAAAACAGAAAGCAGTTTC 9633
QY 291 ThrSerVal-----LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeu 307
Db 9634 AAGCATTTAATTTAAAGTAATCAAAATTTCTTCCAGGTGAG-----AAACTTA 9687
QY 308 GluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPhe 327
Db 9688 GTGGAGACCGCTTTGAAATGAGTGAATAAATGTT-----CAACACATTAAGTG 9738
QY 328 SerSerAsnAsp-----IleGlyGlnArgIleGluLeuSerAspGly---Thr 342
Db 9739 GACAAATTAAGATGTACTATTCCTCCCAAAAGATGTGGCTTACAAAAAGGGAACGC 9798
QY 343 TyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPhe 362
Db 9799 TATACATTAAGTGAAGTAAGAACGACCTGACGACATGATAGCAAGAAAGACTTGG 9858
QY 363 LysValGlnAla-----GlyLysValTyrThrIleLeuAspGlyLysGlnIleGlu 379
Db 9859 CAATTGAGGTGAGTGACGCAAGCAAAAGTA-----AGCATGATGACAAAGAGTACC 9912
QY 380 AsnProAsnLysGluIleValGluProTyrSerValGlnAlaLysAsnAspPheGlu 399
Db 9913 ACCAACAATCAAGTAT-----CCATTGGAATTCGA-----AATTAATTTCTTCT 9960
QY 400 PheSerVal-----LeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLys 415
Db 9961 TTGCAATCAGATTTGAATAATACCATGCAAAAT-----GGCAAA 10002
QY 416 AsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProP 435
Db 10003 CAAGTGAACCTTACGACAGCGGACTTTGCTTGCACAAAGAA----- 10042
QY 435 AspSerSerGluAspGlyLysThrMetThrProAspPheThrThrGlyGluValLysTyr 455
Db 10043 -----AAAAATGCTGCAAGAGAACTTACCAAACTGTGGCAACTGAAA 10083
QY 455 TrpHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspPr 475
Db 10084 AACAGATACACAGAGATGAGCTATTTT----- 10111
QY 475 AspThrPheLeuLysHisIleLysLysValIleGluLysGly---TyrArgLysGln 494
Db 10112 -----AAAAATTAAGTGAACCGTGGAGTATACGA----- 10138
QY 494 GlnAlaIleGluTyrSerGlyLeuThrGlnLeuArgAlaIleThrGlnLeuAl 514
Db 10139 -----ATGCTGGAACAATCAGAA-----CCATTAGGCTACGACCTTGTCTGG 10182
QY 514 aileTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGln 534
Db 10183 AATTTATGAATTTACT-----GTTGATAAA----- 10207
QY 534 yPheGlyAspMetAsnAspSerThrLeuAlaValIleLeuValGluTyrAlaGln 554

```

```

Db 10208 -TATGGAAA-----ATTCACTATGCAGG 10230
Qy 554 n-----AsperasnpProGlnLeuThAspleuasphetheleProasnas 571
Db 10231 CAAAAATATTGAAAGAAATGGCCGATGAGCA----- 10264
Qy 571 nasLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGlnAspleuValaspileI 591
Db 10264 ----- 10264
Qy 591 earGmetGlnAspLysGlnValIleProValThrHisasnLeuThrLeuArgLys-- 610
Db 10265 -----CTGCACATCAAAATATTGAAACCTTT 10293
Qy 611 -----ThyValThrGlnLeuAlaGlyAspArgThrLysAspPheHisPheGluIleG 628
Db 10294 TGACTTAACAGTATATATAAAAAAGCCGATATACAGACG-----CC 10332
Qy 628 uLeuLysasnAsnLysGlnGlnLeuLeuSerGlnThrValLysThrAspLysThrAsnle 648
Db 10333 ACTTAAAGAGCGCAAAATTCCTTTACAGCA-----CCAGATACGAGATAT 10377
Qy 648 uGluPhe---LysAspGlyLysAlaThr-----IleasnLeuLysHisG 662
Db 10378 TGAATTTACCAAAAGATGGCAAAAGAACGATCTTTGTTGAAAACCTTAAACCCAG 10437
Qy 662 yGlu---SerLeuThrLeuGlnGlyLeuProGlnGlyTyrSerTyrLeuValLysGluTh 681
Db 10438 GAAATATGTTCTTACAGAAACCTTTACGCCAGAAAGATATCAGGGCTTAAAGAACCAAT 10497
Qy 681 rAsp-----serGlnGlyTyrLysValLysValasnSerGlnGlnValAlaAsnAl 698
Db 10498 CGAATTAATTAATTCGTGAAGATGGTTCAGTCACGATGATGGGAAAAGTAGCAGATGT 10557
Qy 698 aThrValSer-----LysThrGlyIleThrSerAspGlnThrLeuAlaPheGluAs 715
Db 10558 TTTAATTTCTGGAGAGAAAGATATCAATTAATCTTACAGCTTACG-----AACCA 10608
Qy 715 nasnLysGlnProValValProThrGlyValAspGlnLysIleasnGlyTyrLeuAlaLe 735
Db 10609 AGCAAAAGTCTTCTTACCTGAACCTGGCGATAGACGCTTGGCTTACTGATGATAGC 10668
Qy 735 uIle-----ValIleAlaGlyLysSerLeuGlyIle 745
Db 10669 GATTAGTACATTCGTGATAGCGGCTGTTATCTCTTATTT 10708

RESULT 8
US-09-070-927A-45
: Sequence 45, Application US/09070927A
: GENERAL INFORMATION:
: APPLICANT: Charles A. Kunsch
: Steven Barash
: Patrick J. Dillon
: TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
: NUMBER OF SEQUENCES: 982
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII Text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/070.927A
: FILING DATE: 04-May-2000
: CLASSIFICATION: <unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/046,655

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: FILING DATE: 1997-05-16
: APPLICATION NUMBER: 60/044,031
: FILING DATE: 1997-05-06
: APPLICATION NUMBER: 60/066,009
: FILING DATE: 1997-11-14
: ATTORNEY/AGENT INFORMATION:
: NAME: Kenley K. Hoover
: REGISTRATION NUMBER: 40,302
: REFERENCE/DOCKET NUMBER: PB369
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15614 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-070-927A-45

Alignment Scores:
Pred. No.: 3,46e-05 Length: 15614
Score: 196.00 Matches: 165
Percent Similarity: 35.57% Conservative: 89
Best Local Similarity: 23.11% Mismatches: 245
Query Match: 4.97% Indels: 216
DB: 15 Gaps: 41

US-09-494-297-2 (1-757) x US-09-070-927A-45 (1-15614)
Qy 88 PheargValAlaHisAspleuArgValasnLeuGlnGlySer-----ArgSerTyrGln 105
Db 9047 TTCAGGTTCACAAACATTA-CCAGAAAGTGCCTTACAGCGCCTACATTAATTAATGATAG 9105
Qy 106 ValTyrCysPheasnLeuLysLysAlaPheProLeuGlnSerAspSerSerValLysLys 125
Db 9106 ATTAT-----TTGGGTAAAGGCGAAGAAATTCAAATT 9138
Qy 126 TrpTyrLysLysHisAspGlyIleSerThrLysPheGluAsp----- 139
Db 9139 CATTAATCAAGTACGT-----ATTCAACACAGATCAAAACCTCAACGTATTTGG 9192
Qy 140 TyrAlaMetSerProArgIleThrGlyLysGlnLeuasnGlnLysLeuArgAlaValMet 159
Db 9193 TATCAAAATGAATGCGGACACAGCTTTCAGCCATTAGCCACGCCCTGAAAGATTCAT 9252
Qy 160 TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGlnGlyLeuGlnProLeuAsnAla 179
Db 9253 TTT-----GGGTTCTCTGGGAAAGCACCT-----GGC 9282
Qy 180 IleargValThrGlnGlnAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsnPro 199
Db 9283 GTGAAGTTAAACGTGAAAAAATCTGGGAAGAGTATGATCAAGACCCGACAAAGTCGGCA 9342
Qy 200 AspGlnSerPheLysArgGlnSerGlnSerAsnLeuValSerThrSer----- 215
Db 9343 GATAATGTGATTTGAAATTAATAGTAAGAAAGCAATGACACAGCCAACTGCAAACT 9402
Qy 216 -----GlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeu 232
Db 9403 GGGTATATTAAATATACAAACAGAAATATGATACCAATAGTTGGAGCGCAAAAT 9462
Qy 233 AlaThrLysMetProLysGlnValProAspAspPheGln-----LeuSerIlePheGln 250
Db 9463 GTAACCCACTTTCCAAACCGCGGATGAAGATCAAGAGTTCTTGGGCTTCCCAA 9522
Qy 251 SerGlnAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeu 270
Db 9523 TACAACAATCAAGACGACAGCTTCAAT-----TATCAAAACACCCGTAATTAGCA--- 9573
Qy 271 ValProThrLysProProThrProGlnLysProPrometProProAsnGlnProGlnThr 290

```

Db 9574 GTTCCTGGTTACAGTCAAGAAAAAATCGAGATCTACTTGGAAAAACAGAACGAGTTC 9633  
 QY 291 Thrserval-----leuilearglytyrallaleglyasptyrserlyleu 307  
 Db 9634 AAGCCATTGATTTAAAAAGTATCAAAAATTTCTCCAGGTGG-----AAAACCTTA 9667  
 QY 308 gluglyalathrleuglnleuthrglyaspasnvalasnsrphneglnlaargvalphe 327  
 Db 9688 GTGGAGACCGCTTGAATTGAGTGAATAAATGTT-----CAACACACTTGTG 9738  
 QY 328 SerSerasnsp-----lleglyluarglleuglnleuSeraspgly---Thr 342  
 Db 9739 GACAAATAAGTGTACTTCTTCCTCCAAAGATCGCGCTACAAAAAGCGAACGC 9798  
 QY 343 TyrThrleuthrgleuasnserproalaglytyrserllealaglnuprollethrphe 362  
 Db 9799 TATACATTAACTGAAGTAAAGACCTGCAGACATAGTTAGCAAGAAAAAGCACTGG 9858  
 QY 363 lysvalgluila-----glylysvaltyrthrilleaspglysglnileglu 379  
 Db 9859 CAATGTGAGTGTAGTGCAGCAAGCAAGTA-----AGCATGTGATGACAAAGTGAAC 9912  
 QY 380 AsnProasnlysgluilevalgluprottyrservalglualaatyraasnaspheglu 399  
 Db 9913 ACCACAATCAAGTTAT-----CCATTGCAAAATTGAA-----AATTAATTTCTCT 9960  
 QY 400 Pheserval-----Leuthrthrlnasntyrallalyspheytyrtyralys 415  
 Db 9961 TTGGCAATCAGAAATTGAATAATACCATGCATAAT-----GGCAAA 10002  
 QY 416 AsnlyshasnlyserSer-GlnvalvaltyrcyspheasnalaaspleuylsSerPropr 435  
 Db 10003 CAAGTGAACTTACAGACAGCGACTTTCCTGCAAAAGAA----- 10042  
 QY 435 oaspsersglaspelyglylysthmethrproasphethrthrclgluvallysty 455  
 Db 10043 -----AAAATGCGCAAGCAAGAGTTACCAACTGGCAACTCAAAA 10083  
 QY 455 rthrhisileaglyAArgspheuphellytyrthrvallysprargspthrpr 475  
 Db 10084 AACAGATACTACAGAGATGTAGCTATTTT----- 10111  
 QY 475 oaspthrphleuylshisileuylsvalillegluylsgly---tyrarggluylsgl 494  
 Db 10112 -----AAAATTAGTGAACCTGCGAGATGCA----- 10138  
 QY 494 yglinalaleglutyserglyleuthrglnuargalalathrglnleual 514  
 Db 10139 -----ATGGTGGAAACATCAGGA-----CCATTAGGCTACGACACTCTTGCTGG 10182  
 QY 514 ailetyrtyrphethrAspsersalagluasnsplyasplyleuylsasptryrhsgl 534  
 Db 10183 AATTTATGATTTACT-----GTTGATAAA----- 10207  
 QY 534 yrhneglyaspmeLasaspserserthrleualavalalalysilleuvalglutyrallagl 554  
 Db 10208 -TATGGGAAA-----ATTGACATATGACAG 10230  
 QY 554 n-----AspSerAsnprothrglnleuthraspleuasphetheleproasnas 571  
 Db 10231 CAAAAATATTGAAGAAAATGCCGCAAGATGGACA----- 10264  
 QY 571 nasnlystyrglnserleuileglythrghlntrhisprrgluaspleuvalaspillell 591  
 Db 10264 ----- 10264  
 QY 591 eargmetsgluasplylsgluvalleprovalthrhisasnleuthrleuarglys-- 610  
 Db 10265 -----CTGACACATCAAAATATTTGAACCTTT 10293  
 QY 611 -----Thrvalthrclyleuvalaglyaspargtthrlyasasphethisheclulegl 628  
 Db 10294 TGACTTTAACAGTTAATAAAAAACCGATATACAGAG-----CC 10332

QY 628 uleuylsasnasnlysglnleuSerleuSerGlnThrVallysthrasplysthra 648  
 Db 10333 ACTTAAAGAGACCGAAATTCGTTTACACAGA-----CCAGATACGAGATAT 10377  
 QY 648 ugluPhe---LysaspelyllysalaThr-----lleasnleuylshsgl 662  
 Db 10378 TGAATTACCAAAAGATGCAAGAAACGATACTTGTGTTTGCAAAACCTTAAACACAG 10437  
 QY 662 yglu---SerleuthrleuglnleuProgluglytyrSerlyleuVallysglu 681  
 Db 10438 GAATATATGTTCTTAACAAACCTTTACCGCAAGAGATATCAGCGGTTAAAGAACCAAT 10497  
 QY 681 rasp-----Sercluglytyrlysvallyasnserclngluvalalasn 698  
 Db 10498 CGAATTATATTCGTGAAGATGTTTCAGTCACGATGATGAGGAAAAAGTACAGATGT 10557  
 QY 698 arthrvalser-----LysthrclglylethrSeraspcluthrleualaphecluas 715  
 Db 10558 TTTAATTCTGAGAGAGAATAATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 10608  
 QY 715 nasnlysgluProvalValprothrclglyvalaspgluylleasncllytyrleualale 735  
 Db 10609 AGCAAAAGTTCCTTTACTGAAACCTGGTGCATAGACGCGCTTGCTTTACTTGATAGC 10668  
 QY 735 uile-----ValillealaglyleSerleu 745  
 Db 10669 GATTAGTACATTCGTGTATACGGGTGTTTATCTTATT 10708

RESULT 9  
 US-60-045-649-1048  
 : Sequence 1048, Application US/60045649  
 : GENERAL INFORMATION:  
 : APPLICANT: Lagace, Robert E.  
 : APPLICANT: Corely, Neil C.  
 : APPLICANT: Russo, Frank D.  
 : APPLICANT: Hann, Amy L.  
 : TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS  
 : TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF  
 : NUMBER OF SEQUENCES: 1466  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 : STREET: 3174 PORTER DRIVE  
 : CITY: PALO ALTO  
 : STATE: CALIFORNIA  
 : COUNTRY: USA  
 : ZIP: 94304  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/60/045, 649  
 : FILING DATE:  
 : CLASSIFICATION:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: CERRONE, MICHAEL C.  
 : REGISTRATION NUMBER: 39,132  
 : REFERENCE/DOCKET NUMBER: PM-0003P  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (415) 855-0555  
 : TELEFAX: (415) 845-4166  
 : INFORMATION FOR SEO ID NO: 1048:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 7971 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA  
 : IMMEDIATE SOURCE:  
 : CLONE: EF1c1048  
 : US-60-045-649-1048



QY 689 sValAsnSerGlnGluValAlaAsnAlaThrValSer-----LysThrGlyLeuH 706  
 Db 3133 GATAGATGGGGAAGAAAGTACAGATGTTTAATTTCTGGAGAGACAAATATATCAATTAC 3192  
 QY 706 rSerAspGluThrLeuAlaPheGlnAsnLysGluProValValProThrGlyValAs 726  
 Db 3193 TTTAGACGTTAGC-----AACCAAGCAAGGTTCTTACTGTAAGCATTCGATGCGGTGTTATCT 3243  
 QY 726 pGlnLysIleAsnGlyTyrLeuAlaLeuIle-----ValIleAlaGlyIleSerIe 743  
 Db 3244 AGGACCGCTGTGTTACTTACTTACTGATAGCATTCGATGCGGTGTTATCT 3303  
 QY 743 uGlyIle 745  
 Db 3304 CTTTATT 3310

RESULT 10  
 US-60-046-653-1042  
 ; Sequence 1042, Application US/6004653  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lagace, Robert E.  
 ; APPLICANT: Corley, Neil C.  
 ; APPLICANT: Russo, Frank D.  
 ; APPLICANT: Hann, Amy L.  
 ; APPLICANT: Heath, Joe D.  
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS  
 ; TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 1449  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/60/046, 653  
 ; FILING DATE: HERewith  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CERONE, MICHAEL C.  
 ; REGISTRATION NUMBER: 39,132  
 ; REFERENCE/DOCKET NUMBER: PM-0003-1 P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 855-0555  
 ; TELEFAX: (415) 845-4166  
 ; INFORMATION FOR SEQ. ID NO: 1042:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8040 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; IMMEDIATE SOURCE:  
 ; CLONE: EFALC1042  
 ; US-60-046-653-1042

Alignment Scores:  
 Pred. No.: 3.32e-05 Length: 8040  
 Score: 192.00 Matches: 172  
 Percent Similarity: 33.65% Conservative: 78  
 Best Local Similarity: 23.15% Mismatches: 220  
 Query Match: 4.87% Indels: 274  
 DB: 58 Gaps: 42

US-09-494-297-2 (1-757) x US-60-046-653-1042 (1-8040)

QY 88 PheArgValAlaHisAspLeuArgValAsnLeuGlySer-----ArgSerTyrGln 105  
 Db 1718 TTACGTTCAACATTA-CCAGAGGTGCTGACAGCGGCTACATTAATGATATGAG 1776  
 QY 106 ValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerValLys 125  
 Db 1777 ATTAT------TTGGTAAGGCGCAAAATTCAAATT 1809  
 QY 126 TrpTyrLysLysHisAspGlyIleSerThrLysPheGlnAsp- 139  
 Db 1810 CATTATCAAGTACGT-----ATTCAACAGAGTCAAGAACTCAACCTGATTTTGG 1863  
 QY 140 TyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMet 159  
 Db 1864 TATCAATGATGATGCTGGACACAGTTTCAGCCATTAGCCAGCGCCCTGAAAAAGTTGAT 1923  
 QY 160 TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAla 179  
 Db 1924 TTT-----GGGTTCTTCGGGAAMACACT-----GGC 1953  
 QY 180 IleArgValThrGlnGluAlaValTyrTyrTyrSerAspAsnAlaProIleSerAspPro 199  
 Db 1954 GTGAGCTTAACCTGAAAAAACTGCGAAGAGTATGATCAAGACCCGCAAGTCGGCA 2013  
 QY 200 AspGluSerPheLysArgLysGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeu 219  
 Db 2014 GATAATGTGATTATGAATTAATGATAGAACCAAGTAACTGACACACCAAC----- 2064  
 QY 220 MetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGln 239  
 Db 2065 TGGCAACAGTGGTATATTAATTAATCAAAACGAAATGATCCGCAATAGTTGGAG 2124  
 QY 240 ValProAspAspPheGlnLeuSerIlePheGluSerGluLysGlyLysPylsTyrAsn 259  
 Db 2125 CGCAAAAATGTAAACCACTTTCACAAACCGCGATGAA----- 2163  
 QY 260 LysGlyTyrGlnAsnLeuSerGlyGlyLeuValProThrLysProThrProGly 279  
 Db 2164 ---AGTATCAACAAGATTCTTGG----- 2184  
 QY 280 AspProPheMetProProAsnGlnProGlnThrThrSerValLeuIle-----Ar 296  
 Db 2185 -----CTTCCCAATATACAAATCAAGACAGCTTCATTAATCAACCAACCGC 2235  
 QY 296 GlyTyrAlaIleGlyAspTyrSer----- 304  
 Db 2236 TGAATTAGCATTCCTGTTACAGTCACAGAAAAATCGACGATCTTGGAAAAACAC 2295  
 QY 305 -----LysIle 306  
 Db 2296 GAGCAGTTCACCCATTAGATTTAAAGTAATCAAAATTTCTCCTCAGGTGAGAAAAA 2355  
 QY 306 uLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgVa 326  
 Db 2356 CTTAGTGAGGAGCGCTTGAATGAGGTAAAAATGTT-----CAAAACAATT 2406  
 QY 326 LysSerSerAsnAsp-----IleGlyGluArgIleGluLeuSerAspGly-- 341  
 Db 2407 AGTGACAAATAAAGATGATGATCTTCTGCAAAAGATGCGGCTCAAAAAAGGGA 2466  
 QY 342 -ThrTyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleH 361  
 Db 2467 AGCCTATACATTATGAGTAAAGTAAACACCTGAGACATGATGGCAAGAAAGCGAC 2526  
 QY 361 rPheLysValGluAla-----GlyLysValTyrThrIleIleAspGlyLysGlnI 378  
 Db 2527 TTGGCAAAATTGAGGTGATGAGCAAGCAAGTA-----AGATGATGAGCAAGAAAGT 2580  
 QY 378 eGluAsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheG 398  
 Db 2581 GACCAACCAACAAGATTAATT-----CCATTGGAATTTGAA-----AATTAATTTTC 2628  
 QY 398 uGluPheSerVal-----LeuThrThrGln-----AsnTyrAl 409

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Db      2629 TTCTTGGCAATGAGATTAGAAATACACCATGCAAAATGCAACAAGTAACTTACG 2688
Oy      409 alyspheThyTyrAla-----LysAnLysAnGlySerSerGlnValValTyrCy 426
Db      2689 AGAGCGCATTTTGGTTGCAAGAAAAAATGCTCAAGAGTTTACCAACGTGTGGCAAC 2748
Oy      426 sPheAsnLAspleuLysSerProProAspSerGlnuSpGlyGlyLysThMetThrPr 446
Db      2749 TCAAAAAACAGAT 2761
Oy      446 oAsPheThrThrGlnValLysTyrThrHisIleAlaGlyArgAspLeuPheLysTy 466
Db      2762 -----ACTACAGA----- 2770
Oy      466 rThValLysProArgAspThrAspProAspThrPheLeuLysHisIleLysValIl 486
Db      2771 -----TTGAGCTATTTT---AAATTAG 2790
Oy      486 eGluLysGly---TyrArgGluLysGlyGlnAlaIleGluTyrSerGlyLeuThGluTh 505
Db      2791 TGAACCTGTGATATGCA-----ATGGTGAGACAATCAGA----- 2827
Oy      505 rGlnLeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAs 525
Db      2828 -CCATTAGCTACGACACTCTTGGCGAAATTATGATTTACT-----GTTGA 2874
Oy      525 pLysAspLysLeuLysAspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaVa 545
Db      2875 TAAA-----TATGGGAAA----- 2887
Oy      545 lAlaLysIleLeuValGluTyrAlaGln-----AspSerAsnProGlnLeuTh 562
Db      2888 -----ATCTACTATGCGAGCAAAAATTTAAGAAAATGGCCAGATGAGC 2934
Oy      562 rAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGlnTr 582
Db      2935 A----- 2935
Oy      582 pHisProGlnAspLeuValAspIleIleArgMetGlnAspLysGluValIleProVa 602
Db      2936 -----CT 2937
Oy      602 lThrHisAnLysLeuThrLeuArgLys-----ThrValThrGlyLeuAlaGlyAspAr 619
Db      2938 GACACATCAAAATTAATTTGAAACCTTTGACTTACAGTTCATATAAAAAACCGATATCA 2997
Oy      619 gThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLysSerG 639
Db      2998 GACG-----CCACTTAAGAGAGCGAAATTCGCTTACACAGGA-- 3034
Oy      639 nThrValLysThrAspLysThrAsnLeuGluPhe---LysAspGlyLysAlaThr----- 656
Db      3035 -----CCAGATACGGATATGTAATACCAAAAGTGTGCAAAAGAACCGATAC 3081
Oy      657 -----IleAsnLeuLysHisGlyGlu---SerLeuThrLeuGlnGlyLeuProG 672
Db      3082 TTTTGTTTTGAACCTTAACCAAGGAAATGCTTACACAGAAACCTTTACGCCGAGA 3141
Oy      672 uGlyTyrSerTyrLeuValLysGluThrAsp-----SerGlnGlyTyrLysVally 689
Db      3142 AGGATATCAGGGGTTAAAGAAACCAATGATTAATATGCTGAAGATGGTCACTCAC 3201
Oy      689 sValAsnSerGlnGluValAlaAsnAlaThrValSer-----LysThrGlyIleTh 706
Db      3202 GATGATGAGGAGAAAGTAGACAGATGTTTAATTTCTGAGAGAGAAATATCAATATAC 3261
Oy      706 rSerAspGluThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAs 726
Db      3262 TTTAGACGTTACG-----AACCAAGCAAAAGGTTCTTTACTGGAACGTGGGCGCAT 3312
Oy      726 pGlnLysIleAsnGlyTyrLeuAlaLeuIle-----ValIleAlaGlyIleSerIle 743

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Db      3313 AGGACGCTGTGCTTTACTGTATGACGATAGTACATTCGTGATAGCGGCTGTATCT 3372
Oy      743 uGlyIle 745
Db      3373 CTTTAT 3379

RESULT 11
US-60-068-217-919
; Sequence 919, Application US/60068217
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert E.
; APPLICANT: Corley, Neil C.
; APPLICANT: Russo, Frank D.
; APPLICANT: Hann, Amy L.
; APPLICANT: Heath, Joe D.
; APPLICANT: Finney, Gregory L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS
; TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
; NUMBER OF SEQUENCES: 1239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/068,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PM-0003-5 P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 919:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11907 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
; IMMEDIATE SOURCE:
; CLONE: EFALC919
; US-60-068-217-919

Alignment Scores:
Pred. No.: 5,48e-05 Length: 11907
Score: 192.00 Matches: 172
Percent Similarity: 33.65% Conservative: 78
Best Local Similarity: 23.15% Mismatches: 220
Query Match: 4.87% Indels: 274
DB: 60 Gaps: 42

US-09-494-297-2 (1-757) x US-60-068-217-919 (1-11907)
Oy      88 PheArgValAlaHisAspLeuArgValAsnLeuGluGlySer-----ArgSerTyrGln 105
Db      5455 TTCAGGTTCACAAACATTA--CCAGAACTGTGCTAACAGCGCTACATTAATGATATGAG 5513
Oy      106 ValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLys 125
Db      5514 ATTAT-----TTGGTAAGGCGCAAGAAATTCAAATT 5546
Oy      126 TrpTyrLysLysHisAspGlyLysSerThrLysPheGluAsp----- 139

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Db 5547 CATTATCAAGTACGT-----ATTCAACAGAGTCAGAAAACTTCAAACTGATTTTGG 5600  
 QY 140 TyrlameterProArgileThrglyAspGlueuasnInlysleuArgAlaValMet 159  
 Db 5601 TATCAATGAATGTCGACACAGCTTTCAGCCATTCAGCCAGGCCCTGAAAAAGTTGAT 5660  
 QY 160 TyrsnInghsProGlnasnlAAsnglylleMetGluGlyleuGluProLeuAsnAla 179  
 Db 5661 TTT-----GGGCTTCCTCGGAAAAAGCACCT-----GGC 5690  
 QY 180 IleArgValThrgIngluAlaValTrpTyTryserspAsnAlaProIleSerAsnPro 199  
 Db 5691 GTGAAGTTAAACGTGAAAAAAATCTGGAGAGATATATCAAGACCGACAGCAAGCGGCA 5750  
 QY 200 AspIuserPheLysArgIuserGluSerAsnleuValSerThrsersGlnLeuSerLeu 219  
 Db 5751 GATTAATGTGATTTATGAATTTAGTACAAAGCAAGTACTGACACAGCCAAC----- 5801  
 QY 220 MetArgGlnAlaLeuLysGlnLeuIleAspProAsnleuAlaThrlYsMetProLysGln 239  
 Db 5802 TGGCAAACTGGGTATTTAATTTATCAAAACAGAAATGATACCAAGCAATAGTTGGAG 5861  
 QY 240 ValProAspAspPheGlnLeuSerIlePheGluSerGluAspLysGlyAspLysTyraSn 259  
 Db 5862 CGCAAAAATGTAAACCCAACTTCCAAAACCGCGGATGA----- 5900  
 QY 260 LysGlyTyTrGlnAsnleuLeuSerGlyGlyleuValProThrlYsProProThrProGly 279  
 Db 5901 ---AGCTATCAAGAAAGTTCTGGG----- 5921  
 QY 280 AspProMetProProAsnGlnProGlnThrservalLeuIle-----Ar 296  
 Db 5922 -----CTTCCCAATCAACAAATCAAGACAGCTTTCATTTATCAAAACACCCG 5972  
 QY 296 GlySTyAlaIleGlySptYser----- 304  
 Db 5973 TGAATTAGCAGTCTCGTTACAGTCAAGAAAAATGACAGACTACTTGGAAAAACAC 6032  
 QY 305 -----LysLe 306  
 Db 6033 GAACAGTTCAGCCATTAGATTAAAAAGTAAATCAAAATTTCTTCAGAGTCGAGAAAA 6092  
 QY 306 uLeuGluGlyAlaThrlLeuGlnLeuThrglyAspAsnValAsnSerPheGlnAlaArgVa 326  
 Db 6093 CTTAGTGGAGCCGCTTTGAAATGAGTGAATAAATGTT-----CAAAACACATT 6143  
 QY 326 lPheSerSerAsnAsp-----lleGlyGluArgIleGluLeuSerAspGly-- 341  
 Db 6144 AGTGCACAAATGAAGATGTAGCTATTCCTGCCAAAAAGATGTGGCCTACAAAAAGGGA 6203  
 QY 342 -ThrTyTrThrlLeuThrgInleuAsnSerProAlaGlyTyTrSerlleAlaGluProIleTh 361  
 Db 6204 ACCGTATACATTAACCTAAAGTAAAGCACCCTGACGACATGATGACCAAGAAACGAC 6263  
 QY 361 rPheLysValGluAla-----GlyLysValTyTrThrllelleAspGlyLysGlnI 378  
 Db 6264 TTGGCAAAATGAGGTGAGTGAAGCAAGCAAGTA-----AGCATCATGAGCAAGAAGT 6317  
 QY 378 eGluAsnProAsnLysGluIleValGluProTyTrSerValGluAlaTyraSnAspPheG 398  
 Db 6318 GACCACCAAAATCAAGTTAT-----CCATTGGAATTAAGAA-----AATTAATTTTC 6365  
 QY 398 uGluPheSerVal-----LeuThrlThrgIn-----AsnTyAl 409  
 Db 6366 TTCTTTGCCAATCAGATTTAGAAAATACACCATGCAAAATGGCAACAACTGAACCTTAGC 6425  
 QY 409 aLysPheTyTrAla-----LysAsnLysAsnGlySerSerGlnValTyrcy 426  
 Db 6426 AGAGCGACATTTGCTTGCAGAAAAGAAAATGCTCAAGGAAGTATACAAACTGAGCAAC 6485  
 QY 426 sPheAsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrlMetInPr 446  
 Db 6486 TCAAAAAACAGAT----- 6498

QY 446 oAspPheThrlThrgInleuValLysTyTrThrlleAlaGlyArgAspLeuPheLysTy 466  
 Db 6499 -----ACTACAGA----- 6507  
 QY 466 rThValLysProArgAspThrlAspProAspThrlPheLeuLysHisIleLysLysValI 486  
 Db 6508 -----TTGAGCATTTT-----AAATTAG 6527  
 QY 486 eGluLysGly---TyraArgLysGlyGlnAlaIleGluTyTrSerGlyLeuThrgInTh 505  
 Db 6528 TGAACCTGGTACGATGAGTGA-----ATGCTGCAACATACAGA----- 6564  
 QY 505 rGlnLeuArgAlaAlaThrgInleuAlaIleTyTrTyPheThrsersAlaGluLeuAs 525  
 Db 6565 -CCATTAGCTACACACACTCTCTGCTGGAANTATGAAATTTACT-----GTTGA 6611  
 QY 525 pLysAspLysLeuLysAspTyTrHisGlyPheGlyAspMetAsnAspSerThrlLeuAla 545  
 Db 6612 TAAA-----TATGGGAAA----- 6624  
 QY 545 lAlaLysIleLeuValGluTyAlaGln-----AspSerAsnProProGlnLeuTh 562  
 Db 6625 -----ATTACATATGACAGCGCAAAATATTTGAAGAAAATCGCCAGAAATGAC 6671  
 QY 562 rAspLeuAspPhePheIleProAsnAsnLysTyTrGlnSerLeuIleGlyThrgInTr 582  
 Db 6672 A----- 6672  
 QY 582 pHisProGluAspLeuValAspIleleArgMetGluAspLysGluValIleProVa 602  
 Db 6673 -----CT 6674  
 QY 602 lThrlHisAsnleuThrlleuArgLys-----ThrlValThrgInleuAlaGlyAspAr 619  
 Db 6675 GACACATCAAAATTAATTTGAACCTTTGACTTAACAGCTTCATTAATAAAACGATATATCA 6734  
 QY 619 gThrlYsAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnleuLeuSerG 639  
 Db 6735 GAGC-----CCACTTAAAGAGCGCAAAATTCGCTTAACAGCA-- 6771  
 QY 639 nThrlValLysThrlAspLysThrlAsnleuGluPhe---LysAspGlyLysAlaThr--- 656  
 Db 6772 -----CCAGATACGATATTGAAATTAACCAAAAGATGGCAAAAGCGATAC 6818  
 QY 657 -----lleAsnleuLysHisGlyGlu---SerLeuThrlleuGlnleuProG 672  
 Db 6819 TTTTGTTTTGAAAACTTAACACCGAGGAATATGTTCTTAACAGAAACCTTTACGCCAGA 6878  
 QY 672 uGlyTyTrSerTyTrleuValLysGluThrlAsp-----SerGluGlyTyTrLysVal 689  
 Db 6879 AGCATATCAGCGGTAAAGAACCAATCAATTAATTAATTCGTAAGATGCTTACAGCAC 6938  
 QY 689 sValAsnSerGlnleuValAlaAsnAlaThrlValSer-----LysThrglyIleTh 706  
 Db 6939 GATAGATGGGGAAGAAATAGACAGATGTTTAAATTTCTGAGAGAACAAATATCAATATAC 6998  
 QY 706 rSerAspGluThrlleuAlaPheGluAsnAsnLysGluProValProThrglyValAs 726  
 Db 6999 TTTAGACGTTAGC-----AACCAAGCAAAAGTTCTTACCTGAAACTGTGGCAT 7049  
 QY 726 pGlnLysIleAsnGlyTyTrleuAlaLeuIle-----ValIleAlaGlyIleSerLe 743  
 Db 7050 AGCAGCGCTTGCTTTACTTACTGATAGGATTAATGATACATTGCTGATACGGGTGTTATCT 7109  
 QY 743 uGlyIle 745  
 Db 7110 CTTTAT 7116  
 RESULT 12  
 US-09-663-779-1301  
 : Sequence 1301, Application US/09663779  
 : GENERAL INFORMATION:



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; APPLICANT: Corbin, David R.
; APPLICANT: Malvar, Thomas M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CHROMOSOMAL GENOME SEQUENCES AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 38-21(51376)B
; CURRENT APPLICATION NUMBER: US/09/663,779
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 1999-09-17
; NUMBER OF SEQ ID NOS: 8283
; SEQ ID NO 1301
; LENGTH: 10627
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; US-09-663-779-1301

Alignment Scores:
Pred. No.: 0.000176 Length: 10627
Score: 185.50 Matches: 132
Percent Similarity: 38.448 Conservative: 104
Best Local Similarity: 21.508 Mismatches: 209
Query Match: 4.708 Indels: 169
DB: 29 Gaps: 32

US-09-494-297-2 (1-757) x US-09-663-779-1301 (1-10627)

OY 208 GUSERASnLeuValSerThSerInLeuSerLeuMetArgInAlaLeuLysGlnLeu 227
DB 3989 GAAATGAAATGCTGGATACAGGGAATGTAGAGATA----- 4024
OY 228 IleAspProAsnLeuAlaThrPlyMetProLysGlnValProAspAspPheGlnLeuSer 247
DB 4025 -----ACAAAATACATTAAGATAGTAAGCTCCATTAGAAAATGTT 4066
OY 248 IlePheGlnUserGluAsp--LysGly-----AspLysTyr 258
DB 4067 GTATTGGAAGTACGCGATTAAAGCAAAAGTATTGCAAAAAGTAAACGCGATTAAAGA 4126
OY 259 AsnLysGlyTyrGlnAsnLeuLeuSerGly-----LeuValProThrLysPro 275
DB 4127 GCAAAAGCAAAAGCTTTCAGATTATTCATTGCAAAAGTATGATGATGAGAACTAGAAACA 4186
OY 276 ProThrProGlyAspProPheProAsnGlnProGlnInThrThrsValLeuIle 295
DB 4187 CCGCGAGATACAAACCACTGCAAAAGCAATTTATTGCAATTTGAAAAGGATGAGATA 4246
OY 296 ArgLysTyrAlaIleGlyAspTyrSerLysLeuGlnGlyAlaThrLeuGlnLeuThr 315
DB 4247 ACAGCATTCACATTCGCTGTAAGAAATGATATTAGTACGACGAAAGTATGAAATTTACA 4306
OY 316 -----GlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspIle 332
DB 4307 AAAGTAGATAAAGAAATTAAGATGCTTTAGCTGATGACGCTTTGAAATTCAGATGCA 4366
OY 333 GlyIuArgIle-----Glu 337
DB 4367 GCAGGACAAAGTAGTCCTAAATTAACGACAGATAAAAAAGCAACGACACTTCTAAT 4426
OY 338 LeuSerAspGlyThrTyrThrLeuThrGluLeuAsnSerProAlaGlyTyr--SerIle 356
DB 4427 TTATCAGTCGCGACATACAGTTAGTACAGTAAGTAAGCAACCAAAAGATATTAACAATTA 4486
OY 357 AlaGluProIleThrPheLysValGluAlaGlyLysValTyrThrIle-----Ile 373
DB 4487 GTAGTCGCGATTTACTTCCTCAATTCGAAATGCAAAAGCGACACAAATCTCTGCTTAAACAGTA 4546
OY 374 AspGlyLysGlnIleGluAsnProAsnLysGluIle-----ValGluProThrSerVal 391
DB 4547 GAAAGCAAAATGTTAGACAAGGAAATGCTGGAAGTACAAAAGTATGATTAAGATAGTCA 4606
OY 392 GluAlaTyrAsnAspPheGluGluPheSerValLeuThrThrGlnAsnTyrAlaLysPhe 411
DB 392 ----- 411

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DB 4607 AAAGCATTTA----- 4615
OY 412 TyrTyrAlaLysAsnLysAsnGlySerSerGlnValTyrCysPheAsnAlaAspLeu 431
DB 4616 -----GCAGTGTAGCTTC----- 4630
OY 432 LysSerProProAspSerGlnAspGlyGlyLysThrMetThrProAspPheThrThrGly 451
DB 4631 -----GAAGTACAAAGCAACAGCAAGCAAGTATGACAA-----GAAGTACGACAGAT 4678
OY 452 GluValLysTyrThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArg 471
DB 4679 AAAGAAAGGAAAGCAAAATATCAGACTATCTGAGCAAACTAC----- 4723
OY 472 AspThrAspProAspThrPheLeuLysHisIleLysLysValIleGluLys----- 488
DB 4724 -----AAATGTAGAGCAAAAGCTTA 4747
OY 489 ---GLYTYRARGGluLysGlyGlnAlaIleGluTyr-----SerGlyLeuThrGlu 504
DB 4748 CCAGGTTCAAAACCACTAACAGAGCCAGTATGCAAAATTTAAAGGCTATGACAGCA 4807
OY 505 Thr---GlnLeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPheThrAspSerAlaGlu 523
DB 4808 GCTTATGATTTAAAGTAGAAGATGACAGATGACAAAGCTTTAGTAAATCACAANA 4867
OY 524 LeuAspLysAspLysLeuLysAspTyrHisGly-----PheGlyAspMetAsnAspSer 541
DB 4868 GTAGATTAAGATGATGCAAAAGTATGAGAGCGAGTCTTGAAGTACAAAGTAAAGAAA 4927
OY 542 ThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnProProGlnLeu 561
DB 4928 GCGCAAGTAGTACAAAGTATACAGACAGAT-----AAAGAAAGCAAAAGCAAGAT 4978
OY 562 ThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGln 581
DB 4979 GCTGATTTATACGTA-----GCAAAATATTAAG---CTAGTACAGGTAGAG 5020
OY 582 TrpHisPro-----GluAspLeuValAspIleIleArgMetGluAspLysGluVal 599
DB 5021 ACCTTACAGAGATATTAAGAACTAGCGAAACCGATATCTTTGAAATCAAAAAA----- 5074
OY 600 IleProValThrHisAsnLeuThrLeuArg----- 609
DB 5075 ---GGTATGACGAAGCTTTATCACTAAAGTAGAAGATGAACTAGTACAAAGGCTCA 5131
OY 610 LysThrValThrGlyLeuAlaGlyAspArgThrLys-----AspPheHisPheGlu 626
DB 5132 GTAGAAATATCACAAGAGTGTAGATAGTCAAAAGATATTTAGAAAGCTAGTCTTCGAA 5191
OY 627 IleGluLeuLysAsnAsnLysGlnLeuLeuSerGlnThrValLysThrAspLysThr 646
DB 5192 GTGCA-----GACGACACAGAAAGTAAGTACGAGATGAAACAGAT----- 5236
OY 647 AsnLeuGluPheLysAspGlyLysAlaThrIleAsn----- 658
DB 5237 -----AAAAATGTAAGCAAAATCTCAGACTTCTGTAGCAAAAGTACAA 5284
OY 659 LeuLysHisGlyGluSerLeuThr--LeuGlnGlyLeuProGluGlyTyrSerTyrLeu 677
DB 5285 TTAGTAGAAGAAAGAGAGCTTACAGGCTACAAAACATTAACAGAGCAGTATCATTCGAA 5344
OY 678 ValLysGluThrAspSerGluGlyTyrLysValLysValAsnSerGlnGluValAlaAsn 697
DB 5345 ATTAAGAAAGGATATGACAGAAAGCTTATCATTTAAAGTAGAAGATGACAGTACACAA 5404
OY 698 AlaThrValSerLysThrGlyIleThrSerAsp-----GluThrLeuAla 712
DB 5405 GGTTCAGTAGTAAGATACAAAGTATGATTAAGTATGACAAAAGTATTGACAAAGCGGTAGTC 5464
OY 713 PheGlu-----AsnAsnLysGluProValValProThrGlyValAspGlnLysIleAsn 730
DB 5465 TTCGAAGTAGCAAGACAGCAAAAGCAAGTAGTA---ACAGAGTAAAGAAACAGATTAAGAT 5521

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QY 731 GlyTyrLeuAlaLeuIleValIleAlaGlyIleSerLeuGly 744  
 Db 5522 GGT-----AAAGTAAATACTCAGACTTATCTGAGCA 5554

RESULT 13  
 US-10-417-884-864  
 : Sequence 864, Application US/10417884  
 : GENERAL INFORMATION:  
 : APPLICANT: Lynn A Doucette-Stramm and David Bush  
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
 : ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
 : NUMBER OF SEQUENCES: 7310  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 : STREET: 100 Beaver Street  
 : CITY: Waltham  
 : STATE: Massachusetts  
 : COUNTRY: USA  
 : ZIP: 02354  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: CD-ROM ISO9660  
 : COMPUTER: PC  
 : OPERATING SYSTEM: <Unknown>  
 : SOFTWARE: ASCII  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/10/417,884  
 : FILING DATE: 17-Apr-2003  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/107,532A  
 : FILING DATE: 30-Jun-1998  
 : APPLICATION NUMBER: 60/085,598  
 : FILING DATE: 14 May 1998  
 : APPLICATION NUMBER: 60/051571  
 : FILING DATE: July 2, 1997  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Arinello, Pamela Deneke  
 : REGISTRATION NUMBER: 40,489  
 : REFERENCE/DOCKET NUMBER: GTC-012  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (781)893-5007  
 : TELEFAX: (781)893-8277  
 : INFORMATION FOR SEQ ID NO: 864:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 2187 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: circular  
 : MOLECULE TYPE: DNA (genomic)  
 : HYPOTHEICAL: NO  
 : ANTI-SENSE: NO  
 : ORIGINAL SOURCE:  
 : ORGANISM: Enterococcus faecium  
 : FEATURE:  
 : NAME/KEY: mIsC-feature  
 : LOCATION: (b) LOCATION 1...2187  
 : SEQUENCE DESCRIPTION: SEQ ID NO: 864:  
 : US-10-417-884-864

Alignment Scores:  
 Pred. No.: 4.73e-05 Length: 2187  
 Score: 182.00 Matches: 155  
 Percent Similarity: 34.82% Conservative: 103  
 Best Local Similarity: 20.92% Mismatches: 238  
 Query Match: 4.61% Indels: 245  
 Db: 52 Gaps: 40

US-09-494-297-2 (1-757) x US-10-417-884-864 (1-2187)

QY 72 TrpTyr-----GlyTyrGluSerTyrValArgIleHis-ProTyrTyr 85  
 Db 468 TGGTACTCTTCTCAGCTCAGAGCTGTGGGACAGTCTTAC---AAGGCTACTCCA----- 519

QY 85 rlySGlnPheArgValAlaHisAspLeuArgValAsnLeuGluLysr-----Argse 103  
 Db 520 -----TCATTTCATAGCAAGAAATACCATCAAGAG 551  
 QY 103 rTyrGlnValTyrCysPheAsnLeuLysValAlaPheProLeuGlySerAspSerSer 123  
 Db 552 CAATCAGATCTAT-----TTAGCAAAACCAAGCAAAAT 584  
 QY 123 llySGlSerTyrTyrLysHisAspGlyIleSerThrLysPheGluLysPyr----- 140  
 Db 585 CCAATCCATTACCAAGTGCAGCA-----ATCCAAACAGAAATAGAGCATTCATCCAA 638  
 QY 141 -----AlaMetSerProArgIleThrGlyAspGluLe 151  
 Db 639 TTTCGTGATCAATAGAACGGCAGACAGACTTTCACCAACTTATACATGATAT 698  
 QY 151 uasnglLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIle 171  
 Db 699 AGCTGAA-----TTCGGTATATCC 716  
 QY 171 tgluGlyLeuGluProLeuAsnAlaIleArgValThrGlnGluAlaValTyrTyrse 191  
 Db 717 ATCTGTAAGCTCCGAGTCACTCTACATC-----AAAAAGTTATGGAGAAT 770  
 QY 191 rAspAsnAlaProIleSerAsnProAspGlu---SerPheLysArgLysSerGluSerAs 210  
 Db 771 TGACAAACAATCTACCTATGCTCCAGATCAAGTACTTTGACATTCACAGCGAA----- 825  
 QY 210 nleuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleAsp 230  
 Db 826 -----CATACGCAAAATGCTGCAGCTTGCAAAACGGAATATTCGAATCATTAAC 878  
 QY 230 oasnLeuAlaThr-----LysMetProLysGlnVa 240  
 Db 879 ACCTAAAGATACCAAAATACGTGCGAAGCTGCAGACATTGCAAAATATCTGCACATAG 938  
 QY 240 lProAspAspPheGln-----LeuSerIlePheGluSerGluAspLysGlyAspLys 258  
 Db 939 CGGAGAAAGTTATCAACAAGATATTATACACCTCAATACAAATACAGTCAAGAT 998  
 QY 258 rAsnLysGlyTyrGlnAsnLeuSerGlyGlyLeuValProThrLysProThrPr 278  
 Db 999 CAGT-----TACCAACAATC-----AAAGAAATTACTCTGACC 1031  
 QY 278 oGly-----AspProPromeProAsnGlnProGlnThrPrse 292  
 Db 1032 AGCATACGATTCACAAATAGATGCAATGACATGCAAAATATCTAAACATTCACACC 1091  
 QY 292 rVal-----LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeuGlu 309  
 Db 1092 GTTAACCTGAAATATACGAAATATCTCTACAGTGAA-----AAGATCTTATATG 1145  
 QY 309 yAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAla---ArgValPhe 328  
 Db 1146 CGGTGTTTCAAAATTAACAGAGATTCATTGATACTTACTTAACAAGATCAGCGCAG 1205  
 QY 328 rSerAsnAspIleGlyLysArgIleGluLeu---SerAspGlyThrTyrThrLeuThr 347  
 Db 1206 AACCTATTCCTTCACAGAAATATGCAATATGCAAAAGAAATACCTATACGCTGACAGA 1265  
 QY 347 uLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAla 367  
 Db 1266 AACCAAAAGCTCCAGAGGCGATGATTAACCAAAAGACACACTTGGGAATCAAGATCG 1325  
 QY 367 yLysValTyrThrIle---IleAspGlyLys----- 376  
 Db 1326 TTCTGATGTACGCTAACCATTCATGATGAGAAACAGTCACTACTTCGATGATACGATCA 1385  
 QY 377 -----GlnIleGluAsnProAsnLysGluIleGluProTyrSerValGluAlaTyrAs 395  
 Db 1386 GTTGACTATATGAATAATCTTTTGTGAAGTT-----CTGTACGATGATGATGAATG 1439  
 QY 395 nasPheGluGluPheSerValLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAla 415

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Db      1440 GATGCAAGGAGGACGACAAAGATTAATCTTAAGAGACACATTTTCCCTACGAAAA 1499
Qy      415 SASNLySAsnclYserSerGlnValValTyrCysPheAsnlaAspLeuLysSerPro 435
Db      1500 AGAAGCAAAATGCTACTTATCAG-----CCAAAT 1526
Qy      435 oAspSerGlu-----AspGlyGlyLysThrMetThrProAspPheThrThrlGlyl 452
Db      1527 TGACAGCCCAACAAACGAATGAAAGGCTTCCACGATTTCATTCACACACCTGCTAA 1586
Qy      452 uValLysTyrThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArg 472
Db      1587 ATATCGAGTCGTTGAACAGCTGGCTCCGCGGATAT-----GA 1625
Qy      472 pThrAspProAspPhePheLeuLysHisIleLysValIleGlyLysGlyTyrArgG 492
Db      1626 TACTTCGCGGGAATATGAAATTCCAATTCGAATGAATAT----- 1665
Qy      492 uLysGlyGlnAlaIleGlyTyrSerGlyLeuThrGlnThrGlnLeuArgAlaIleThrG 512
Db      1666 -----GGAAAAATCATT--TACAGGGGAAAAAATACGAGATGACAAATTAATGATGAC 1718
Qy      512 nLeuAlaIleTyrTyrPheThrAspSerAlaGlyLeuAspLysAspLysLysAspTy 532
Db      1719 GCTCAGTCATCAAAATGACATAAAGCGTTGATCTACGCTACACAAAGAAAGAAC-- 1776
Qy      532 rHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGly 552
Db      1777 -----AACGGACAGCATTTAAAGACCAAAATTCAGACCTGCAG-- 1815
Qy      552 rAlaGlnAspSerAsnProGlnLeuThrAspLeuAspPheIleProAsnAsnAs 572
Db      1816 -----GGACCAAGAAATG--GACTTACAA----- 1836
Qy      572 nLysTyrGlnSerLeuIleGlyThrGlnThrHisProGlnAspLeuValAspIleIle 592
Db      1837 -----TCGCCAAAGAT----- 1848
Qy      592 gMetGlnAspLysLysGlnValIleProValThrHisAsnLeuThrLeuArgLysThr 612
Db      1848 ----- 1848
Qy      612 lThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeuLysAsn 632
Db      1849 -----GGACAAGAACAGATACCTTCTATTCGAA----- 1878
Qy      632 nLysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGlnPheLys 652
Db      1878 ----- 1878
Qy      652 pGlyLysAlaThrIleAsnLeuLysHisGlyGlu--SerLeuThrLeuGlnGlyLeu 671
Db      1879 -----AATTTAAACCTGGAACCTTATACGCTGACCGCAACCTTTTACACC 1922
Qy      671 oGluGlyTyrSerTyrLeu-----ValLysGluThrAspSerGluGlyTyrLysVal 688
Db      1923 AGAAGGATACCAAGCTTAAGAGAGCCAGTTACTATACATACACGAAAGATGGGTCAAT 1982
Qy      688 lLysValAsnSerGlnGluValAlaAsnAlaThrValSerLysThrGlyIleThrSer 708
Db      1983 TCAAGTGCATGACAAAGT-----CATGAATCTGTTGTGCACAGGAGCCAAAAACAA 2036
Qy      708 pGlu--ThrLeuAlaPheGluAsnAsn--LysGluProValValProThrGlyValAs 726
Db      2037 CCAGATTTCTTTACATCAGATCAGCAATGCAAAAGTACATTAACCTGAAGGGAGCAAT 2096
Qy      726 pGlnLysIleAsnclYtyrLeuAlaLeuIleValIleAlaGlyIleSerLeuGlyIle 746
Db      2097 TGCCCGTTAGCAATCTAT-----CTAGTAGGATGATGTTGTGCGTTTCTATTTG 2150
Qy      746 p 746

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Db      2151 G 2151
RESULF 14
US-09-600-720-17
; Sequence 17, Application US/09600720
; GENERAL INFORMATION:
; APPLICANT: GUSSE, Bengt et al.
; TITLE OF INVENTION: NOVEL FIBRONECTIN-BINDING PROTEIN
; FILE REFERENCE: 0825-0161P
; CURRENT APPLICATION NUMBER: US/09/600,720
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 17
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Streptococcus equi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (108)..(1901)
US-09-600-720-17

Alignment Scores:
Pred. No.: 6,84e-05 Length: 2127
Score: 180.00 Matches: 150
Percent Similarity: 34.64% Conservative: 98
Best Local Similarity: 20.95% Mismatches: 270
Query Match: 4.56% Indels: 198
Db: 26 Gaps: 33

US-09-494-297-2 (1-757) x US-09-600-720-17 (1-2127)
Qy      68 SerGluTyrArgTyrTyrGlyTyrGlnSerTyrValArg--GlyHisProTyrTyrLys 86
Db      201 GCAGAGCAGCTTATATGATGCGAATGATGACAGCAAGTTCGCCATATTTT--- 257
Qy      87 GlnPheArgValAlaHisAspLeuArgValAsnLeuGlyLysArgSerTyrGlnVal 106
Db      258 ---TTGTACGTAATGCCCTAAAGATGCTCCAAAGCGTGAAATTAAGACAGATGTTGTT 314
Qy      107 TyrCysPheAsnLeuLysLysAlaPheProLeuGlnLysSerAspSerSerValLysTyr 126
Db      315 TATTCCTTTAACAAAAAATTTGATTTGGCCAGATCATGGAATCATATATACAGCAATTTT 374
Qy      127 -----TyrLysLysHisAspGlyIleSer 134
Db      375 AATGACATCAGATCTCCATATACGATTTACCTGATATGAGAAAAAATAGATATGAT 434
Qy      135 ThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAspGlnLeuAsnGlnLys 154
Db      435 GGTATATTTTAAACAATATATGCTCCAGATTACAAAAAAGATATTATGATATTCACAGTCT 494
Qy      155 LeuArgAlaValaMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGly--- 173
Db      495 TTGCGGCAAGTTTAAAGTAATGATACATACCCCACTAACAGTCAACATCTCAACTGCTAC 554
Qy      174 ---LeuGlnProLeuAsnAlaIleArgValThrGlnGlnAlaValTyrTyrTyrSerAsp 192
Db      555 CATTTAAATATGATTTCTTACAAAGAACTACTCAATTAAGCAATTTGGTATTTTATAGTGAT 614
Qy      193 AsnAlaProIleSerAsnProAspGlnSerPheLysArgGlnSerGlnSerAsnLeuVal 212
Db      615 -----AGTTTAACAAGAAATACCTTAAAGATACGCGGTATTAATACCTTA--- 659
Qy      213 SerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeu 232
Db      660 -----AACGATATGCAAAAAAACCTTTAGCTTTTATTAATCAGTAAGAGAGAG 707
Qy      233 AlaThrLysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGluSerGln 252
Db      708 GATTCCTAAGCTT---AAATCAGACAGAGTAATTAATCATGATGATTTATTTATCAAA 764
Qy      253 AspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValPro 272

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Db 765 AGTGGCGGCGATGACCATATGAAAGATTACCAAAATCTCTCGGCTTACCTTAATTCCT 824
QY 273 ThrLysProProThrProGlyAspProPrometProProAsnGlnProGlnThrSer 292
Db 825 AAAGAACCCTGTAAGCTT
QY 293 ValLeuIleArgLysThrAlaIleGlyAspTyrSerLysLeuGluGlyAlaThrLeu 312
Db 843 -----CAGCTAGGTGCTTTAGT----- 860
QY 313 GlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspIle 332
Db 861 -----GGACATATGAAATGATTAAGCGGCTTGAGAGAGATCATGACGCTCA 911
QY 333 GlyGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrGluLeuAsnSerProAla 352
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QY 353 GlyTyrSerIleLeuGlu-----ProIleThr-----PheLysValGluAlaGly 367
Db 960 GGACTCTCAGAGAACGAGGCGCAACGAGATCCTTGCCAGAGATTGAAGGCTGAGCTGCT 1019
QY 368 LysValIleThrIleIleAspGlyLysGlnIleGluAsnProAsnLysGluIleValGlu 387
Db 1020 GCACCTGATACA-----CCTCAAAAGCCTAATGATTCATTG----- 1055
QY 388 ProTyrSerValGluAlaTyrAsnAspPheGluGluPheSerValLeuThrGlnAsn 407
Db 1056 -----CAAGGCTTCAAGCGGCTTAC-----TCTCTATAGTAGAACAAC 1097
QY 408 TyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValValTyrCysPhe 427
Db 1098 TATGTAGT-----ACCGAAGATATCATGTCATCAGCAGCATCTGTAG----- 1142
QY 428 AsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrMetThrProAsp 447
Db 1143 GAAACCGAAGATACTAACCACCTGATCATCTAGCGCGCTCAGAAATGTGCA----- 1199
QY 448 PheThrThrGlyLysValLysTyrThrHisIleAlaGly-----Arg 461
Db 1200 -----ACCATGAGATACCTAACAACCTCATCTATGGGAGATCGCGCGGCTAGCTGCC 1256
QY 462 AspLeuPheLysTyrThrValLysProArg-----Asp 472
Db 1257 GAATCAGAGAAACGACCTTAACACGACAAACCGCGGCGGACAGACCATGATCAG 1316
QY 473 ThrAspProAspThrPheLeuLysHisIleLysLysValIleGluLysGlyTyrArgGlu 492
Db 1317 ACAACAGAGATACA-----CAA 1334
QY 493 LysGlyGlnAlaIleGluTyrSerGlyLeuThrGlnLeuArgAlaIleThrGln 512
Db 1335 AAGGATGCTGTGCAAAATCTGCTGCACATGAGTCAAGAAACCAAAACCCGAG 1394
QY 513 LeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyr 532
Db 1395 GTCATGATTGCTGTGAGGACAAACATGACAGACAAACAGAGACACACAAAA----- 1448
QY 533 HisGlyPheGlyLysPheLysAspSerThrLeuAlaValAlaLysIleLeuValGluTyr 552
Db 1449 -----GGCATGCTGCAATCTGGCGGTACTATGAG----- 1481
QY 553 AlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPheIleProAsnAsnAsn 572
Db 1482 TCGAGAGACACTAAGAAACCTGAGTC----- 1508
QY 573 LysTyrGlnSerLeuIleGlyThrGlnThrPheLysProGluAspLeuValAspIleIleArg 592
Db 1509 -----ATGATTGGTGTGAG----- 1523
QY 593 MetGluAspLysLysGluValIleProValThrHisAsnLeuThrLeuArgLysThrVal 612

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Db 1524 -----GGACAAATCATGACTCTCTGAAAC-----ACCAATCAGGTATG 1565
QY 613 ThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeuLysAsnAsn 632
Db 1566 TCTGGGAGTGTGTGTGACACTACG-----GTAAATGAG----- 1598
QY 633 LysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPheLysAsp 652
Db 1599 -----GATACCAAGAGCTGAGTAAATCATTTGTCGGG 1631
QY 653 GlyLysAlaThrIleAsnLeuLysHisGlyGluSerLeuThrLeuGlnGlyLeuProGlu 672
Db 1632 CAAGGCAAAATCATGCACTTCTCTGAGGATACACGCGGCTATGTCGTGCT-----CAATCT 1688
QY 673 GlyTyrSerTyrLeuValLysGluThrAspSerGluGlyLysValLysValAsnSer 692
Db 1689 GAGAGCCTACATATGTGCGAGACACCAAGACCCGACCTTAAGCTTAACCTGCACCT 1748
QY 693 GlnGluValAlaAsnAlaThrValSerLysThrGlyIleThrSerAspGluThrLeuAla 712
Db 1749 GCGCCATATGTTAAT-----GACGAA----- 1769
QY 713 PheGluAsnAsnLysGluProValProThrGlyValAspGlnLys----- 728
Db 1770 -----AAACCTAACAAGCCTCATCTCCACAGACAAAGTGAATGAAACAACTCACCCTA 1826
QY 729 -----IleAsnGlyTyrLeuAlaLeuIleValIleAlaGlyIleSerLeu 743
Db 1827 AGCATCATGCTGTCATATGATGCTGCTTGTCTATGTCGTCTTA 1874

RESULT 15
US-10-269-017-17
; Sequence 17, Application US/10269017
; GENERAL INFORMATION:
; APPLICANT: GUS, Bengt et al.
; TITLE OR INVENTION: NOVEL FIBRONECTIN-BINDING PROTEIN
; FILE REFERENCE: 0825-0172P
; CURRENT APPLICATION NUMBER: US/10/269, 017
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Streptococcus equi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (108)..(1901)
US-10-269-017-17

Alignment Scores:
Pred. No.: 6, 84e-05 Length: 2127
Score: 180.00 Matches: 150
Percent Similarity: 34.648 Conservative: 98
Best Local Similarity: 20.958 Mismatches: 270
Query Match: 4.56% Indels: 198
DB: 49 Gaps: 33

US-09-494-297-2 (1-757) x US-10-269-017-17 (1-2127)
QY 68 SerGluTyrArgTrpTyrGlyTyrGluSerTyrValArg---GlyHisProTyrTyrLys 86
Db 201 GCAGACAGAGCTTATATGATGAGTGAATGCAAGCAAAAGTCCCATATTTT--- 257
QY 87 GlnPheArgValAlaHisAspLeuArgValAsnLeuGluGlySerArgSerTyrGlnVal 106
Db 258 ---TGTAGCTATCGCTTAAATGCTCCAAAGCGTAATTAAGACAGATATGTTGTT 314
QY 107 TyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLysTrp 126
Db 315 TATTCCTTTAAACAAAATTTGATTTGGCCAGATCAATGGGAATCTTATACAGCAATTTT 374
QY 127 -----TyrLysLysHisAspGlyIleSer 134

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Db 375 AATGACATCAGATCCATATTAACGATTTCCTGTATATGAGAAAAAAGTACGATFATGAT 434
Qy 135 ThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLys 154
Db 435 GGTATATTATTAACAAATATGCTCCAGATTACAAAAGATATATTAGTATATGCAAGTCT 494
Qy 155 LeuArgIleValMetTyrAsnGlyHisProGlnAsnIleAsnGlyIleMetGlnGly--- 173
Db 495 TTGGTGACGTTTAACTAATGATACCCACTACAAAGTCACAACTACATCACTAGCTAC 554
Qy 174 ---LeuGluProLeuAsnAlaIleArgValThrGlnGluAlaValTyrTyrSerAsp 192
Db 555 CATTTAAATATATGATTTCTTCTAGAAAAGTTACTCAATATAGCATTTGGTATTATGAT 614
Qy 193 AsnAlaProIleSerAsnProAspGluSerPheLysArgIleGluSerGluSerAsnLeuVal 212
Db 615 ---AATTAAACAAAAGAAATACCTTAAAGATACGGGTGTTATTAACCTTA--- 659
Qy 213 SerThrSerGlnLeuSerLeuMetArgIleAlaLeuLysGlnLeuIleAspProAsnLeu 232
Db 660 ---AACGATATGGAAGAAAAGCTTTAAGATTTTAACTAAGTAAAGAGAG 707
Qy 233 AlaThrLysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGlnSerGlu 252
Db 708 GATTCCTAAGCTT---AAATCAGACGACAGATTAATTAATGATTTATGATTTATCAAA 764
Qy 253 AspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValPro 272
Db 765 AGTCGGCGCATGCATCATGAAAGATTAACCAAAATCTTCCGGCTCACTTAATTCCT 824
Qy 273 ThrLysProProThrProGlyAspProProMetProProAsnGlnProGlnThrThrSer 292
Db 825 AAAGAACCCTGAAGCTT--- 842
Qy 293 ValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuGluGlyAlaThrLeu 312
Db 843 ---CAGCTAGTGTGTTT--- 860
Qy 313 GlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspIle 332
Db 861 ---GGACATAATGAAATGATTAAGCGCGCTTGAGAGAGATCATCAAGTCA 911
Qy 333 GlyGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrGluLeuAsnSerProAla 352
Db 912 CAAGAAACTAATGAA---GATGTGAAGAAAGACTT---ATAGTTTCCATGGA 959
Qy 353 GlyTyrSerIleAlaGlu---ProIleThr---PheLysValGluAlaGly 367
Db 960 GGACTCTCAGGAAGCGAGGCAAGCAAGATCCTTCCAGATTCGAAGCGTGAGCTGCT 1019
Qy 368 LysValTyrThrIleLeuAspGlyLysGlnIleGluAsnProAsnLysGlyIleValGlu 387
Db 1020 GCACCTGATACA---CCTCAAAAACCTAATGATCCATTG--- 1055
Qy 388 ProTyrSerValGluAlaTyrAsnAspPheGluGluIleHisSerValLeuThrGlnAsn 407
Db 1056 ---CAAGTCTTGAAAGCGGTAC---TCTCCTAATAGTAAGAACAAAC 1097
Qy 408 TyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnAlaValTyrCysPhe 427
Db 1098 TATGTGATG---ACCGAAGATATCATGTCATCATGACCATTCCTTGAG--- 1142
Qy 428 AsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrMetThrProAsp 447
Db 1143 GAAACCGAAGTACTAACCACCTGATCATACTAGCGGCTCAGAAATGTGAA--- 1199
Qy 448 PheThrThrGlyGluValLysTyrThrHisIleAlaGly---Arg 461
Db 1200 ---ACGATGAGATTAAGAACCCCTCATCTGATGGGATCGCGCGGTCTAGCTGCC 1256
Qy 462 AspLeuPheLysTyrThrValLysProArg---Asp 472

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Db 1257 GAATCAGAGAAACGACACTTAACACGACAAACCGCGGCAAGACCATCATCGAG 1316
Qy 473 ThrAspProAspThrPheLeuLysHisIleLysLysValIleGluLysGlyTyrArgGlu 492
Db 1317 ACAACAGAGATACA---CAA 1334
Qy 493 LysGlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaIleThrGln 512
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Qy 513 LeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyr 532
Db 1395 GTCATGATGTGGTGCAGGCAACCAATCATGACAGACACAGAGACACAAACAA--- 1448
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Qy 553 AlaGlnAspSerAsnProProGlnIleuThrAspLeuAspPhePheIleProAsnAsn 572
Db 1482 TCACAGGACACTAAGAAACCTGAGGTC--- 1508
Qy 573 LysTyrGlnSerLeuIleGlyThrGlnThrHisProGluAspLeuValAspIleIleArg 592
Db 1509 ---ATGATTTGTTGTCAG--- 1523
Qy 593 MetLysAspLysLysGluValIleProValThrHisAsnLeuThrLeuArgLysThrVal 612
Db 1524 ---GGACAAATCATGCACTCTCTGAAAC---ACCAATCAGGATG 1565
Qy 613 ThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeuLysAsn 632
Db 1566 TCTGGGAGCTGTGGTGCACATGAC---GTAATTTGAG--- 1598
Qy 633 LysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPheLysAsp 652
Db 1599 ---GATACCAAGAACTTGAGATATATGATGTCGG 1631
Qy 653 GlyLysAlaThrIleAsnLeuLysHisGlyLysSerLeuThrLeuGlnGlyLeuProGlu 672
Db 1632 CAAGGACAAATCATGCACTCTCTGAGGATCTCAGCGGGATATGTCGT---CAATCT 1688
Qy 673 GlyTyrSerTyrLeuValLysGluThrAspSerGluGlyTyrLysValLysSer 692
Db 1689 GGAGGCACTACAAATGTGGAAGACACCAAGAACCGACCTTAAGCTGACACT 1748
Qy 693 GlnGluValAlaAsnAlaThrValSerLysThrGlyIleThrSerAspGluThrLeuAla 712
Db 1749 GCGGCATTTGTTAAT---GACGAA--- 1769
Qy 713 PheGluAsnAsnLysGluProValValProThrGlyValAspGlnLys--- 728
Db 1770 ---AAACCTAACAAAGGCACTCATCTCCACAGCAAGTATATGAAAGCAATCACCCTA 1826
Qy 729 ---IleAsnGlyTyrLeuAlaLeuIleValIleAlaGlyIleSerLeu 743
Db 1827 AGCATTCGCTGCAATGTCAATGCTGCTCTCTATGTCGTCTTA 1874

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Search completed: August 19, 2003, 19:42:41  
 Job time : 4845 secs

